

Identification of tissue/cell specific marker genes and
use thereof

5 **Cross References to Related Applications**

This application claims the priority of US provisional patent application 60/388994, filed June 14, 2002, the disclosure of which is incorporated herein by reference in its entirety.

10 **Field of the Invention**

The present invention relates to a method for the identification of tissue cell specific marker genes, a method for the determination of a disease state or developmental status of cells/tissue as well as to gene expression profiling of cartilage tissue. More specifically, the invention relates to microarrays containing a plurality of selected human chondrocyte specific sequences and their use for classification of cartilage donor tissue or generation of characteristic gene expression profiles of *in vitro* chondrocyte cultures. Such DNA arrays find use as a standard tool of molecular biology research and clinical diagnostics for all cartilaginous or related tissues.

Background of the Invention

Limitation on current microarray technologies

25 DNA array technology, also known as biochip or microarray technology, is currently revolutionizing modern biology. In this technology, a biological sample is applied to a glass slide or chip covered with an array of immobilized DNA probes. Sample nucleic acid complementary to specific probes on the array hybridizes and can be detected with high sensitivity with automated, computerized detectors. In this manner, hundreds to thousands of different individual hybridization experiments can be performed simultaneously. This allows assays of enormous complexity to be carried out – for example, an analysis of the entire gene expression

profile of a cancer cell – with simplicity unimaginable only a few years ago. As a consequence many patents as well as scientific publications have accumulated during the last years. U.S. 6,194,158 discloses characteristic genes and gene expression useful in screening for, diagnosis of, monitoring
5 of, and therapeutic treatment of brain cancer. U.S. 6,218,122 discloses methods for determining or monitoring the progression of disease states or the efficacy of therapeutic regimens within human patients. U.S. 6'077'673 discloses mouse arrays having a plurality of probe polynucleotides corresponding to a key mouse gene for expression analysis of critical
10 mouse genes. A list of representative scientific papers dealing with monitoring the expression level of a large number of transcripts within a cell at any time are as follows: Schena et al., 1995, Quantitative monitoring of gene expression patterns with a complementary DNA-microarray, Science 270: 467-470; Lockhart et al., 1996, Expression monitoring by hybridization
15 to high-density oligonucleotide arrays, Nature Biotechnology 14:1675-1680; Blanchard et al., 1996, Sequence to array: Probing the genome's secrets, Nature Biotechnology 14:1649. Qi et al., 2003, Identification of genes responsible for osteoblast differentiation from human mesodermal progenitor cells PNAS 18;100(6):3305-10. While this list of scientific papers
20 and patents reflects without any doubt the great potential of microarrays, there are a couple of yet unsolved problems that are more and more discussed among the scientific community. Especially, these problems are data overflow, representative sample collection, RNA processing and inappropriate data analysis. It is even suspected that within next five years,
25 many of conclusions drawn from published data will be revised or refuted. Thus there remains a real and unmet need for advanced microarray solutions, targeted to specific tissues above all with respect to simplification and substantiation of the process of data generation and data handling. With respect to this issue the disclosed invention has made considerable
30 contribution in the cartilage area with a cartilage-specific microarray containing a manageable number of cartilage relevant genes.

Limitation on the number of cartilage relevant genes

Until today the number of cartilage-relevant genes (genes that have been associated a potential functional role on cartilage biology, homeostasis or pathology) is very limited. Approximately, 100-200 genes have been described in the literature in any relationship to cartilage tissue. While existing publications e.g. Heller et al PNAS, 94; 2150-2155; 1997 have described analysis of inflammatory diseases of cartilage and Sekiya et al PNAS 99; 4397-4402; 2001 cartilage formation from stem cells with microarrays, a comprehensive analysis and determination of characteristic gene expression profiles for 2D, 3D, fetal, adult and pathological chondrocytes cell cultures cultivated under different conditions has not been performed up to now. While in patent WO01/24833 A2 a few markers have been determined that are associated with chondrocytes and their phenotype stability, it will not be possible to perform a detailed gene expression analysis and to define specific fingerprints. Therefore the possibility of characterizing culture conditions or cartilage tissue samples can not be thoroughly addressed.

Completion of the human genome first project draft on 2000 has revealed that the human genome comprises ~30000-35000 human genes. Estimates show that the number and type of active genes vary significantly between different tissues and may increase up to a couple of 10000 for complex tissues, e.g. brain. As a consequence, many genes albeit fully sequenced may have yet not been disclosed to be functionally up- or down regulated in cartilage or cartilage derived cells. The inventive approach described herein has made possible to up to now disclose a total of 467 known and additional genes being differentially expressed in a significant and objective manner within chondrocytes or chondrogenic cells.

By means of the already known and additionally found to be cartilage related genes, a strategy to best address and represent chondrocytes cultured under different conditions has been developed in the scope of the present invention.

Summary of the Invention

In a first aspect the present invention relates to a method for the identification of tissue/cell specific marker genes comprising

a) taking tissue and/or cells of at least one developmental stage and/or at least one disease state, and/or

cultivating said tissue and/or cells *in vitro* under at least one culture condition,

b) determination of gene expression profiles of said tissue/cells and/or *in vitro* cultivated tissue/cells and

c) identification of specific marker genes by bioinformatic analysis of said gene expression profiles.

In particular, the first aspect relates to a method for the identification of tissue/cell specific marker genes comprising cultivating tissue/cells of different developmental stages and/or health conditions *in vitro* under different culture conditions, determination of gene expression profiles of said *in vitro* cultivated cartilage tissue and identification of specific marker genes by bioinformatic analysis of said gene expression profiles.

In a preferred embodiment said tissue is selected from the group consisting of fetal tissue, adolescent tissue, adult tissue, healthy tissue, pathological tissue, progenitor cells such as stem cells or cells derived from the same precursor lineage. Preferred culture conditions are 2D and 3D *in vitro* cultures and the gene expression profiles are preferably determined by means of a micro-array. The bioinformatic analysis of said gene expression profiles is preferably done by cluster software such as e.g. cluster analysis.

In a preferred embodiment said tissue is cartilage.

A second aspect of the present invention relates to a method for the determination of a disease state or developmental status of cells/tissue or the physiological potential of cells/tissue. Said method comprises establishing a profile of cellular constituents, preferably a gene expression profile, of said cells or tissue, comparison of said resulting gene expression profile with gene expression profiles characteristic for a particular status or physiological potential of the examined cells or tissue.

Said method can e.g. be. used to assess the redifferentiation potential of cells or tissue, the assessment of the quality of tissue biopsies for diagnostic and prognostic purposes regarding *in vitro* tissue engineering applications, the assessment of the quality of *in vitro* produced cells such as e.g. mesenchymal cells, stem cells or embryonic cells or of *in vitro* produced tissue for therapeutical applications and for determining the effect of one or more growth factors, media compositions or drugs on cells or tissue. Based on said method it is e.g. possible to set up different *in vitro* culture conditions for cells/tissue allowing the cultivation of cells/tissue which retain their potential for differentiation.

In a preferred embodiment said cells or tissue is cartilage tissue or chondrocytes and the array comprises polynucleotide probes of tissue specific marker genes.

In a further preferred embodiment said profile is a gene expression profile which is determined by means of a micro-array.

A further object of the present invention is a method for the determination of characteristic profiles for clinical use comprising correlating the patient data of the biopsy donor with the gene expression profile of said biopsy cells/tissue. Preferably said gene expression profile has been determined according to the above disclosed method. The resulting profiles of said method are suitable tools in the clinic allowing an evaluation of further treatments of a patient.

The present invention provides characteristic gene expression profiles experimentally determined by using cartilaginous tissues as from individual human donors of various ages (fetal, adolescent, adult) and health conditions (healthy and arthritic) or cells thereof cultivated under different *in vitro* culture conditions (2D and 3D *in vitro* cultures, time follow ups). From these different gene expression profiles a set of hitherto 467 markers has been deduced that can be used to design and produce a cartilage specific microarray for commercial applications in the field of R&D, such as culture media development, drug screening etc., but also for clinical applications.

Gene expression analysis performed with such microarrays and the corresponding analytical procedure thereof can be used to assess quality control of human donor cartilage, e.g. biopsy and therefore optimization of any downstream tissue engineering process, for diagnostic evaluation of the patient and its candidate treatment methods, to ensure a cost-optimized procedure, to investigate and assess all kind of 2D- and 3D *in vitro* cultures performed with human chondrocytes or chondrogenic cells, e.g. stem cells, to screen all kind of drugs, e.g. hormones, growth factors within the above mentioned *in vitro* cultures regarding a potential beneficial effect and quality assessment of *in vitro* produced tissue performed by tissue engineered procedures.

In a further aspect the present invention provides a cartilage array comprising a plurality of different polynucleotide probe spots stably associated with a solid surface of a carrier, whereby each of said spots is made of a unique polynucleotide that corresponds to one specific cartilage marker gene.

A preferred cartilage array of the present invention comprises at least two spots that have different nucleotide sequences but of the same cartilage marker gene, more preferably at least 10 spots indicative for one tissue or cell status, whereby said at least 10 spots can be selected from different sequences of one gene or from different genes or a combination thereof.

In a preferred embodiment said polynucleotides of the array do not cross hybridize under stringent conditions with each other.

In a preferred embodiment of the present invention the cartilage array comprises spots that are indicative for at least two tissue or cell status, preferably 3.

A further preferred inventive cartilage array is an array wherein at least part of the cartilage marker genes are selected from the 467 genes listed in the description, preferably at least 10 %, more preferably at least 50 %, most preferably about 100 %.

A further preferred inventive cartilage array is an array wherein at least part of the cartilage marker genes are selected from a

subgroup of the 467 genes listed in the description, wherein said subgroup consists of the most tissue specific 200 genes.

In another preferred embodiment the status is selected from biopsies and/or 2D cultures and/or 3D cultures of healthy adult, healthy fetal/infant, undesired adult, undesired fetal/infant or progenitor cells like e.g. stem cells or cells derived from the same precursor lineage.

In a further preferred embodiment of the present invention the polynucleotide probes of the cartilage array have a length of at least 10 nucleotides, preferably at least 20 nucleotides. The probes can also have a length of 30 nucleotides, 50 nucleotides or 70 nucleotides. It is as well possible to use PCR derived products produced from cDNA clones.

In a preferred embodiment the carrier of the inventive cartilage array is attached to coated glass, nylon or any other material.

A further object of the present invention is a kit for use in a hybridization assay, wherein said kit comprises a cartilage array of the present invention. In a preferred embodiment said kit comprises reagents for generating a labelled target polynucleotide sample, a hybridization buffer and a wash medium.

Description of the Figures

The present invention will be further understood from the following description with reference to the tables and figures where:

Tab.I shows the determined number of all genes in the corresponding SOM analysis being differentially expressed according to microarray analyses of a variety of *in vitro* chondrocyte cultures according to predefined criteria. From these data sets specific expression profiles can be deduced that are characterisitic for different cell culture conditions.

Tab.II shows the extracted and reviewed genes deduced from Tab I in order to have only single entry numbers. Since most of these genes have never been described in any relationship to cartilage, they can be considered as novel cartilage marker (positive/negative markers) or key cartilage genes.

Tab III shows a subset of marker genes from Tab. II that has been used for the production of a micro-array. Included is a subset from Tab II and genes known from the literature.

5 Tab IV shows the results of the analysis of the 467 cartilage specific marker genes.

Tab V shows the samples used in Examples 1, 2 and 3. Human chondrocytes isolated from 4 different donors were proliferated and kept in 3D-like pellet culture for 7 and 14 days resulting in a total number of 12 samples.

10 Fig.1 shows a classical result from an analysis performed with self-organizing-maps. This software clusters all genes together in sub clusters that show a similar expression profile. The number of marker genes for the corresponding analysis e.g. 2D vs. 3D cultures (see also Tab I) corresponds to the total number of genes in the sub clusters.

15 Fig 2 shows an example of a graphical presentation of a cluster analysis and viewed by the software treeview. This shows how cells from different origin and potential for *in vitro* cartilage formation are related to each other and allow a clearer classification of the cell sources. Fetal cells clearly produce different gene clusters compared to adult chondrocytes, 20 while failures are characterized by other gene clusters. Furthermore 3D cell cultures analyzed in a time dependent manner from different donors can be distinguished among each other and gene expression profiles will be grouped accordingly.

25 Fig 3: SOM analysis of all culture conditions and samples described in Example 2 and in Tab V.

Fig 4: SOM analysis for proliferated chondrocytes (t0) only, for the 4 donors. Gene expression pattern corresponding to donor 2 (the second spot from left hand side in every cluster) behaves different in most clusters.

30 Fig 5: SOM analysis of chondrocytes kept in 3D culture condition for 7 days (t7). Gene expression pattern from donor 3 (the third spot from left hand side in every cluster) is different for example in clusters c2 and c5.

Fig 6 shows self organized maps (SOM) of chondrocytes from same patients of Figures 4 and 5 kept under 3D culture condition for 14 days (t14).

Fig 7: cluster analysis of all culture conditions and samples described in Example 2 and in Tab V. This figure shows a subset of 88 hierarchical clustered genes (rows) and samples (columns) demonstrating similar gene expression behavior of chondrocytes under different culture conditions. For example proliferated cells (#1, #2, #4, #5, #7, #8, #10, #11) can easily be discriminated from cells kept in 3D-like pellet culture for 14 days (3#, 6#, 9#, 12#).

Fig 8: cluster analysis of human aortic fibroblasts vs. chondrocytes. This figure shows a subset of selected clusters of human aortic fibroblasts cells compared to human chondrocytes both kept in 3D pellet cultures for 14 days. The dendrogram in the upper part of the figure shows the ability of CART-CHIP™ 300 microarray described in this invention to discriminate between different cell lines.

Fig 9: cluster analysis of Interleukin-1 treated vs. untreated human chondrocytes. This figure demonstrates a subset of representative gene clusters allowing differentiation between cells treated with Interleukin-1 from untreated cells both kept in 3D pellet cultures as well as for proliferated cells.

Detailed Description of the Invention

Definitions

2D cultures as used in the scope of the present invention are anchorage dependent chondrocyte cultures cultivated on plastic culture devices.

3D cultures as used in the scope of the present invention are chondrocytes cultured in a three dimensional environment, namely either a) scaffold-free, such as small high density pellet cultures ($0.25\text{--}3.0 \times 10^6$ cells) or as high density cultures using 50×10^6 cells/ml or aliquots thereof; or b) by using a synthetic scaffold such as PGA, PLA, or mixtures

thereof or biological substances such as agarose, alginate, chitosan or collagen.

failures as used in the scope of the present invention are chondrocytes cultured in a three dimensional environment that are not able to synthesize new extracellular matrix thereby compromising the production of new living tissue engineered cartilage equivalents.

gene expression profile as used in the scope of the present invention is a profile of genes that are up or down regulated according to different cell conditions.

fingerprint as used in the scope of the present invention refers to a gene expression profile characteristic for a cellular status.

tissue or cell status as used in the scope of the present invention refers to a tissue or cells thereof having a certain metabolic or activity status.

new extracellular matrix as used in the scope of the present invention designates living cartilage-like tissue.

micro-array as used in the scope of the present invention is used in its original scope that encompasses embodiments today sometimes referred to as "macro-arrays".

The Invention

The present invention provides cartilage-specific gene arrays as well as methods for their use. In the subject cartilage arrays, a plurality of polynucleotide probe spots are stably associated with the surface of a solid carrier, preferably a surface of a microscope glass slide. Each different polynucleotide probe spot is made of a unique polynucleotide that corresponds to a key cartilage gene of interest. Thus, the subject arrays find particular use in gene expression assays of key cartilage genes. In further describing the subject of the invention, the cartilage specific microarrays are first discussed, followed by a review of representative applications in which the subject arrays may be employed.

Arrays of the Subject Invention-General Description**Selection of novel key cartilage specific genes:**

A critical feature of the subject arrays is that all of the probe polynucleotide spots of the array correspond to human key cartilage genes that have been found through unique selection processes and criteria. As a result of said processes, up to now 467 different key human cartilage genes that are under tight transcriptional role have been discovered, some of them being not described before in any relationship to cartilage. In more detail, different microarray analyses were performed by using cartilaginous tissues as from individual human donors of various ages (fetal, adolescent, adult) and health conditions (healthy and arthritic) or cells thereof cultivated under different *in vitro* culture conditions (2D and 3D *in vitro* cultures, time follow ups). This variety of cartilage cell sources and different culture conditions was set up to grasp the highest possible number of genes differentially expressed and thus being indicative of a potential role.

It has been found that specific chondrocyte culture conditions are of great importance for the present invention that discloses a plurality of novel key cartilage genes as well as characteristic and meaningful gene expression patterns. For this reason, the strategy and criteria of the analysed *in vitro* human chondrocyte cultures are described in more detail. The principal experimental setup included both the cultivation of chondrocytes in an anchorage dependent condition, known as 2D cultures for expansion of cells e.g. where the passages is variable but at least more then one, as well as cultivation of chondrocytes in an anchorage independent condition, known as 3D cultures for (re-)differentiation and de novo tissue formation of cells. These are the key steps of any tissue engineering process where autologous tissue equivalents are produced. Since the cell source is either a small biopsy, a small bone marrow aspirate in case of mesenchymal stem cells or other tissue with a limited number of pre-chondrogenic cells, it is first necessary to isolate those cells in order to be able to multiply the cell number drastically. In case of a cartilage biopsy, cells are released from their surrounding extracellular matrix by collagenase digestion and then seeded onto the surface of plastic tissue culture flasks.

The proliferation may take place either in the presence or absence of fetal serum combined with conventional DMEM/F12 medium. Cells can then be passaged by trypsin treatment over several rounds. As a major drawback of this necessary cell expansion, the cells lose their differentiated phenotype and assume a de-differentiated phenotype with altered gene expression. It is further known that with increasing number of passages the state of de-differentiation also advances. As a consequence, genes being transcriptionally upregulated under such artificial culture conditions are cartilage relevant in a manner being indicative of an undesired cellular status. It is also quite common to designate these genes as de-differentiation or negative markers. While healthy tissue in general has been found to re-differentiate in 3D culture after up to 4 passages in 2D cultures, tissue of undesired cellular status cultivated under usual conditions, such as usual culture media, usually does not re-differentiate in 3D culture after at most 4 passages in 2D culture.

Subculture modulated chondrocytes that do not express differentiation markers reexpress the differentiated phenotype in response to the anchorage-independence resulting from various 3D culture models, e.g. high density cultures, agarose or alginate cultures, or cultures within synthetic scaffolds such as made of polyglycolic acid (PGA), polylactic acid (PLA) or mixtures thereof. To set up three dimensional cell cultures the cells are detached after proliferation by trypsin treatment and embedded either in gel-like substances such as alginate, seeded within a porous scaffold such as PGA or cultivated as high-density cultures, only. The time for the analysis may vary and ideally addresses several time points (up to several weeks). Thus 3D *in vitro* chondrocyte cultures support the differentiated phenotype of chondrocytes and can be used to discover cartilage relevant genes or differentiation markers. It should be noted however, that reversibility of the de-differentiation process is dependent on the number of passages and can become irreversible or at least partially irreversible at higher passage numbers (under usual conditions at most about 4 passages). As a rule the time course of de- and re-differentiation are similar. During skeletal development, cartilage serves as a template for

bone formation. Chondrocytes of fetal or infant (< 1 year) or growth plate cartilage pass through different stages and exhibit several distinct phenotypes, such as resting, proliferating, and hypertrophic chondrocytes. Progression through each of these phases is accompanied by profound changes in gene expression patterns. Further, evidence has accumulated that the successful sequence of cartilage repair via tissue engineering recapitulates aspects of embryonic tissue formation. For these reasons, it is important to consider fetal and infant cartilaginous tissue. Cells isolated from human fetal/infant cartilage that are cultivated in 2D and 3D culture systems as described above are especially helpful to understand the mechanisms underlying the phenotypic instability of chondrocytes and the related gene expression patterns. These 2D and 3D culture system may then be analyzed to deduce gene expression profiles and to define marker genes that are characteristic for the (re-)differentiation process. Thus maintenance of chondrocyte-specific phenotype being crucial for normal structure and biomechanical properties of articular cartilage may be better understood and have important implications for modern therapeutic biological applications.

The above mentioned experimental setup for 2D and 3D cultures may be even expanded to compare human adult cells with human fetal/infant chondrocytic cells of age <1 year. The comparison of gene expression profiles of adult versus fetal/infant human chondrocytes during the *in vitro* cartilage formation process is an important aspect since marker genes associated with developmental aspects are revealed. This can be of further interest when 3D cell cultures need to be optimized for their *in vitro* performance for the production of new tissue by e.g. adding growth factors that are found to play a major role during the early onset of cartilage formation *in vivo*.

Another experimental setup found in the scope of this invention includes the *in vitro* culture of cells harvested from cartilaginous areas of arthritic knee joints. Osteoarthritis (OA) results from the failure of chondrocytes within the joint to maintain the balance between synthesis and degradation of extracellular matrix. OA is a multifactorial disorder in

which aging, genetic, hormonal and mechanical factors are all major contributors to its onset and progression. With progressing disease state, the articular chondrocytes ability to maintain homeostasis and functionality is increasingly disappearing. As a consequence, the phenotype of osteoarthritic chondrocytes compared with normal chondrocytes exhibits remarkable changes. Gene expression profiling allows characterization of the osteoarthritic cellular phenotype, a key determinant for understanding and manipulation of osteoarthritic processes. By studying and comparing the gene expression profiles of chondrocytes harvested from pathological and healthy human cartilage areas it becomes possible to identify marker genes that are able to predict the future outcome of cell cultures used for *in vitro* tissue engineering applications. This also relates to the very critical question of the assessment of the quality of the starting biopsy material that is being used for downstream applications like tissue engineering. By having this important information before performing any downstream applications like e.g. proliferation and consecutive 3D *in vitro* tissue formation, the further steps of any process can then be adapted or even not performed at all because of inadequate quality of biopsy material. Such decision may be of high relevance when tissue-engineering processes are transferred or applied in the clinic. Gene expression profiling of chondrocytes may then be used as a diagnostic tool to allow and to choose that therapeutic approach with the most promising clinical outcome.

A further important aspect of the invention is the observation that chondrocytes derived from osteoarthritic patient material always qualify for anchorage dependent proliferation in 2D over several passages. These cells however, if subsequently induced to re-differentiate by culturing them as 3D high density pellets, do not survive over an extended time period, in most cases they die in culture by undergoing apoptosis. It is assumed that these cells, due to an altered phenotype, are not capable of producing the critical survival factors in the appropriate concentrations, above all extracellular matrix components providing intercellular spaces as they occur in native cartilage. Cells that are not suitable to be cultured within 3D high density cultures are herein referred to

as „failures“. These impaired cell cultures can be used to set up representative “failure” systems, where cells from different pathological cartilage sources are harvested, proliferated and cultivated in 3D high density pellet culture systems. After each of these experimental steps, RNA
5 can be isolated from the different cell sources and combined to create “failure pools”. These failure pools are very well suitable to identify general marker genes being indicative of the onset of osteoarthritis.

For finding cartilage relevant genes, and for determining their presence dependent on the specific cartilage type such as age, health
10 etc., sufficient material must be generated, e.g. by 2D culturing over several passages, and optionally 3D culturing. Said material then can on be subjected to usual gene analyses, and the tissue specific genes determined. Cartilage samples are classified prior to culturing and/or after culturing to get the information needed for later interpretation of the gene
15 expression profile.

A further experimental setup of the current inventions discloses the analysis of chondrocytes grown in 3D cultures isolated from pathological human cartilage and analyzed in a time dependent manner. This experimental set-up allows to study the apoptotic process and to
20 further define additional dynamic and characteristic gene expression profiles, useful for deducing and further assessment of the quality of the biopsy material.

The microarray process and strategy for disclosing all the cartilage relevant genes with the above-mentioned tissues and cell culture
25 criteria will be described in the following. An important issue of the inovative strategy used by the inventors of the present inventions is to use various microarrays containing a high number of genes comprising different functional categories preferentially by representing the whole genome. The broader the microarray regarding the coverage of the human genome the
30 more genes associated with chondrocyte cell cultures can be determined. The chosen strategy of the inventors was not obvious to a person skilled in the art.

RNA isolated from the above mentioned different cell cultures conditions may be radioactive labeled with e.g. ^{33}P or fluorescence like e.g. Cy3 and hybridized to the corresponding filters or microarrays. After hybridization each array may then be scanned and the corresponding signals measured (Tab IV). This raw data file needs then to be calibrated and normalized in a manner to create an input file for the further downstream analysis process. In principle if the data are normalized an expression profile is created. To identify the key cartilage marker genes being differentially expressed under the chosen criteria, tedious bioinformatic analysis are conducted. Corresponding cell cultures and their expression profiles are therefore compared and analyzed accordingly and the different clusters of marker genes determined by software analysis e.g. self-organizing maps (herein referred to as SOM). A representative example of a result for the comparison of different gene expression profiles from different cell culture conditions performed by SOM analysis is given in Fig.1. By performing SOM analysis genes that are similarly expressed are clustered together in so-called sub clusters. The total amount of marker genes for one analysis corresponds to the total amount of sub clusters containing the corresponding genes. Table I in the appendix summarize the results of all the different analysis performed and encompasses all the genes determined for every set of cell culture analysis.

By performing this analytical procedure the analysis reveals several characteristic up and down regulated marker genes for different cellular culture conditions. From these marker genes characteristic expression profiles can then be deduced and used as a benchmark for the comparison or further characterization of other cell cultures.

Hence, on the one hand previously unknown cartilage-relevant genes associated with different culture conditions and on the other hand characteristic gene expression profiles (cellular fingerprints) indicative of a stage of development, a disease state or a particular selected cell culture condition are revealed. These fingerprints are part of the current invention and are of major importance for the classification and

characterization of chondrocytes cultivated under different culture conditions.

Since the gene clusters from all the different analysis contain repetitive gene entries, they have been further processed so that only single entry genes are recorded (see Tab II). This 467 selected sequences are thus all key cartilage genes that are activated and thus differentially expressed according to a stage of development, a disease state or a particular selected cell culture condition and are part of the current invention. A list of all 467 genes with their Pubmed accession no. and a description is given below See also Tables II and III):

List of Table II related sequences:

Pubmed Accession No	Description
AA283693	Human osteoclast stimulating factor mRNA, complete cds
AA845156	Serine protease inhibitor, Kazal type 1
R52548	Human superoxide dismutase (SOD-1) mRNA, complete cds
T67128	ARYLAMINE N-ACETYLTRANSFERASE, MONOMORPHIC
AA845015	Elastase 1, pancreatic (elastase IIA)
AA937895	Antigen identified by monoclonal antibodies 12E7, F21 and O13
AA844998	Pancreatic polypeptide
AA844818	Amylase, alpha 2A; pancreatic
AA894557	Creatine kinase B
AA872001	Annexin VI (p68)
H09590	Human mRNA for eukaryotic initiation factor 4A1
AA868278	Testis specific protein 1 (probe H4-1 p3-1)
AA490855	Acid finger protein ZNF173
H05820	Human MRL3 mRNA for ribosomal protein L3 homologue (MRL3 = mammalian ribosome L3)
N57766	Agammaglobulinaemia protein-tyrosine kinase atk
AA873885	Alkaline phosphatase, liver/bone/kidney
AA878880	Interferon (gamma)-induced cell line; protein 10 from
R54818	Human eukaryotic initiation factor 2B-epsilon mRNA, partial cds
AA458630	RENIN PRECURSOR, RENAL
W37864	Phosphatase and tensin homolog (mutated in multiple advanced cancers 1)
N63192	Phenylethanolamine N-methyltransferase
R55789	Human X11 protein mRNA, partial cds
R56871	Human chromatin assembly factor-I p60 subunit mRNA, complete cds
AA448659	M-PHASE INDUCER PHOSPHATASE 2
AA235388	Tropomodulin
W37769	Chromogranin B (secretogranin 1)
AA421701	H.sapiens mRNA for MUF1 protein
N81029	Collagen, type XVIII, alpha 1
AA644128	Nuclear autoantigenic sperm protein (histone-binding)
N26536	ATPase, Cu++ transporting, beta polypeptide (Wilson disease)
AA890663	Human protein kinase PAK1 mRNA, complete cds
AA405987	Glycerol kinase 2 (testis specific)
AA888182	Ribosomal protein S4, X-linked
H09730	Adenylate kinase 2 (adk2)
AA285155	CDC46 HOMOLOG
AA873351	Ribosomal protein L35a
H12320	CAMP-RESPONSE ELEMENT BINDING PROTEIN
AA856556	Ribosomal protein S28
R43581	Human guanine nucleotide-binding protein G-s, alpha subunit mRNA, partial cds
AA633768	60S RIBOSOMAL PROTEIN L24
AA496880	Ribosomal protein L5
AA625632	Ubiquitin A-52 residue ribosomal protein fusion product 1
R40850	H.sapiens mRNA for alpha-centractin
AA486072	Small inducible cytokine A5 (RANTES)
N80129	Metallothionein 1L
T67270	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX SUBUNIT VI REQUIRING PROTEIN
AA775364	60S RIBOSOMAL PROTEIN L30
AA464743	Ribosomal protein L21
AA663983	Triosephosphate isomerase 1
AA634008	40S RIBOSOMAL PROTEIN S23

AA683050	40S RIBOSOMAL PROTEIN S8
AA775874	60S RIBOSOMAL PROTEIN L18
AA029934	Integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
AA872397	GALECTIN-2
AA428195	Protein tyrosine phosphatase, non-receptor type 2
AA478724	Insulin-like growth factor binding protein 6
T40541	H.sapiens mRNA for human giant larvae homolog
N33214	H.sapiens mRNA for membrane-type matrix metalloproteinase 1
W69399	Homo sapiens adenosine triphosphatase mRNA, complete cds
H85454	Homo sapiens delayed-rectifier K+ channel alpha subunit (KCNS1) mRNA, complete cds
T71284	Complement component 1, q subcomponent, beta polypeptide
N95418	Human FK-506 binding protein homologue (FKBP38) mRNA, complete cds
AA430675	Human DNA repair protein XRCC9 (XRCC9) mRNA, complete cds
AA682851	Homo sapiens mRNA for ERp28 protein
AA427433	PROTEIN PHOSPHATASE PP2A, 65 KD REGULATORY SUBUNIT, ALPHA ISOFORM
AA100296	H.sapiens PAP mRNA
AA070997	Proteasome (prosome, macropain) subunit, beta type, 6
R27585	Proteasome component C2
N71628	Spi-B transcription factor (Spi-1/PU.1 related)
AA464566	Human mRNA for LDL-receptor related protein
AA043228	Calponin 3, acidic
AA478273	APEX nuclease (multifunctional DNA repair enzyme)
H05619	Homo sapiens GDNF family receptor alpha 2 (GFRalpha2) mRNA, complete cds
AA405562	Protein phosphatase 4 (formerly X), catalytic subunit
AA147043	Homo sapiens CAGH1a (CAGH1) mRNA, partial cds
AA035384	Homo sapiens mRNA for small subunit of cytochrome b in succinate dehydrogenase complex, complete cds
R60150	Human mRNA for histidyl-tRNA synthetase (HRS)
N64051	Homo sapiens Werner syndrome gene, complete cds
AA405748	SPLICING FACTOR U2AF 65 KD SUBUNIT
AA461110	Homo sapiens growth-arrest-specific protein (gas) mRNA, complete cds
AA845167	ELASTASE IIIA PRECURSOR
AA443118	Homo sapiens mRNA for CD151, complete cds
N92319	Glycoprotein Ib (platelet), beta polypeptide
AA187148	Core-binding factor, beta subunit
AA253413	Friedreich ataxia
AA046701	ATP SYNTHASE LIPID-BINDING PROTEIN P1 PRECURSOR
AA164562	Homo sapiens actin-related protein Arp3 (ARP3) mRNA, complete cds
AA496357	Homo sapiens SKB1Hs mRNA, complete cds
AA180742	TUBULIN ALPHA-4 CHAIN
AA454743	Human protease M mRNA, complete cds
AA437226	Interleukin 10 receptor
AA458849	Homo sapiens placental bikunin mRNA, complete cds
AA504891	Crystallin, alpha B
AA609655	Homo sapiens mRNA for SCP-1, complete cds
AA599158	MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE
AA052932	Homo sapiens casein kinase I gamma 2 mRNA, complete cds
AA789328	Homo Sapiens (clone PK2J) CDC2-related protein kinase (PISSLRE) mRNA, complete cds
AA129537	Human GAP SH3 binding protein mRNA, complete cds
AA486209	Low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1
H39018	H.sapiens Syt V gene (genomic and cDNA sequence)
AA464217	V-akt murine thymoma viral oncogene homolog 1

T95053	Homo sapiens Rigui (RIGUI) mRNA, complete cds
AA454646	LYMPHOTOXIN-BETA RECEPTOR PRECURSOR
AA448400	Human plectin (PLEC1) mRNA, complete cds
H13691	Major histocompatibility complex, class II, DM beta
AA132086	Homo sapiens RCL (Rcl) mRNA, complete cds
AA488073	Mucin 1, transmembrane
N40945	H.sapiens mRNA for DRES9 protein
R55705	Homo sapiens orexin receptor-1 mRNA, complete cds
H50114	Homo sapiens NMDA receptor mRNA, complete cds
AA452841	Human K-CI cotransporter (hKCC1) mRNA, complete cds
W73790	IMMUNOGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR
N30302	POSSIBLE GTP-BINDING PROTEIN HSR1
AA291556	Human ras inhibitor mRNA, 3' end
AA598510	Human APRT gene for adenine phosphoribosyltransferase
AA453787	Human TFIIB related factor hBRF (HBRF) mRNA, complete cds
H05655	Human transcriptional activator mRNA, complete cds
AA419177	INTEGRAL MEMBRANE PROTEIN E16
AA458807	Human retinal protein (HRG4) mRNA, complete cds
AA293218	Cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kD
W44860	Human calmodulin mRNA, complete cds
AA629862	Homo sapiens mRNA for smallest subunit of ubiquinol-cytochrome c reductase, complete cds
AA447674	Homo sapiens HIV-Nef associated acyl CoA thioesterase (hNAACTE) mRNA, complete cds
T52484	Nerve growth factor beta
AA496810	Protein kinase C substrate 80K-H
AA486233	G1 to S phase transition 1
AA079775	TYROSINE-PROTEIN KINASE CSK
W73889	Tetranectin (plasminogen-binding protein)
R50337	Solute carrier family 19 (folate transporter), member 1
R55046	MpV17 transgene, murine homolog, glomerulosclerosis
R46821	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT
R87763	Human telencephalin precursor mRNA, complete cds
H69583	Human BTG2 (BTG2) mRNA, complete cds
R56046	Guanine nucleotide binding protein (G protein), alpha z polypeptide
AA922705	Glycogen phosphorylase B (brain form)
AA487571	Surfactant, pulmonary-associated protein C
AA402440	Homo sapiens exportin t mRNA, complete cds
H29521	ATP-binding cassette 3
AA490911	Homo sapiens drp1 mRNA, complete cds
AA486082	Homo sapiens sgk gene
AA678065	2,3-bisphosphoglycerate mutase
R43509	Human Gu binding protein mRNA, partial cds
N57553	Adenosine receptor A2
AA676955	Aplysia ras-related homolog 12
R14692	Human Na/H antiporter (APNH1) mRNA, complete cds
AA488979	Homo sapiens nucleolar protein (MSP58) mRNA, complete cds
AA443630	Aldehyde dehydrogenase 8
AA027840	H.sapiens mRNA for RIT protein
AA456830	Diacylglycerol kinase, alpha (80kD)
AA453015	H.sapiens L23-related mRNA
AA074446	Human GTP cyclohydrolase I feedback regulatory protein gene, complete cds
AA027042	DNA-DIRECTED RNA POLYMERASE II 23 KD POLYPEPTIDE
AA629923	Human mRNA for pM5 protein
AA460830	Homo sapiens (clone mf.18) RNA polymerase II mRNA, complete cds

AA454218	Homo sapiens transcription factor SL1 mRNA, complete cds
AA046523	H.sapiens mRNA for centrin gene
R51346	Human eIF-2-associated p67 homolog mRNA, complete cds
AA029964	Human ataxin-2 related protein mRNA, partial cds
AA489219	DUTP pyrophosphatase
AA043133	Solute carrier family 16 (monocarboxylic acid transporters), member 1
AA812973	Human mRNA for testis-specific TCP20, complete cds
AA453471	GANGLIOSIDE GM2 ACTIVATOR PRECURSOR
AA284693	Transcription factor AP-4 (activating enhancer-binding protein 4)
N90281	Human B7 mRNA, complete cds
AA629542	Brush-1
AA679345	Human BTK region clone ftp-3 mRNA
H37774	Tuberin
T97181	Platelet factor 4
AA454879	Plasminogen activator, urokinase receptor
AA147640	Phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)
AA757429	Human serotonin N-acetyltransferase mRNA, complete cds
AA490991	Homo sapiens HnRNP F protein mRNA, complete cds
AA422058	H.sapiens mRNA for D1075-like gene
N66208	Human (ard-1) mRNA, complete cds
AA630776	Human AP-3 complex delta subunit mRNA, complete cds
AA827287	Human interferon-induced leucine zipper protein (IFP35) mRNA, partial cds
AA488084	Superoxide dismutase 2, mitochondrial
R89715	Protein kinase C, gamma
AA490501	H.sapiens mRNA; UV Radiation Resistance Associated Gene
N32199	Human melanoma antigen recognized by T-cells (MART-1) mRNA
AA434404	DNA primase polypeptide 2A (58kD)
N93686	Aldehyde dehydrogenase 7
AA292676	Human metargidin precursor mRNA, complete cds
AA464417	INTERFERON-INDUCIBLE PROTEIN 1-8U
AA442092	Catenin (cadherin-associated protein), beta 1 (88kD)
AA026644	Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)
AA481464	Peptidylprolyl isomerase B (cyclophilin B)
T68859	Alpha-2-plasmin inhibitor (alpha-2-Pi)
AA699560	Surfeit 1
AA705069	Human mRNA for receptor of retinoic acid
AA457739	Homo sapiens putative OSP like protein mRNA, partial cds
H99843	Homo sapiens mRNA for quinolinate phosphoribosyl transferase, complete cds
AA399410	Signal transducer and activator of transcription 3 (acute-phase response factor)
AA443039	HEAT SHOCK 70 KD PROTEIN 1
AA164440	Human autoantigen pericentriol material 1 (PCM-1) mRNA, complete cds
AA446453	Human mRNA for c-myc binding protein, complete cds
AA280692	Diacylglycerol kinase delta
AA031514	Matrix metalloproteinase 7 (matrilysin, uterine)
R33154	Msh (Drosophila) homeo box homolog 1 (formerly homeo box 7)
AA487452	Human DNA fragmentation factor-45 mRNA, complete cds
AA400329	Human gene for neurofilament subunit M (NF-M)
AA454668	Prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
AA486393	Cytokine receptor family II, member 4
R52541	unknown EST
AA171613	Homo sapiens carbonic anhydrase precursor (CA 12) mRNA, complete cds
AA235706	Human TATA-binding protein associated factor 30 kDa subunit (tafil30) mRNA, complete cds
AA668527	Human mucosal addressin cell adhesion molecule-1 (MAdCAM-1) mRNA, complete

	cds
T54144	Homo sapiens homolog of the Aspergillus nidulans sudD gene product mRNA, complete cds
R14080	Calcium modulating ligand
AA609599	Homo sapiens SSX3 (SSX3) mRNA, complete cds
AA489201	H.sapiens mRNA for PHAPI2b protein
R08876	Human 26S proteasome-associated pad1 homolog (POH1) mRNA, complete cds
H46425	H.sapiens Pur (pur-alpha) mRNA, complete cds
R56149	Human putative transmembrane protein (nma) mRNA, complete cds
AA454619	Homo sapiens mRNA for Hic-5, partial cds
H15445	H.sapiens mRNA for SEX gene
AA705225	Myosin, light polypeptide 4, alkali; atrial, embryonic
AA191488	Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds
N64862	Human SLP-76 associated protein mRNA, complete cds
R45413	Human transmembrane 4 superfamily protein (SAS) mRNA, complete cds
R77293	Intercellular adhesion molecule 1 (CD54), human rhinovirus receptor
AA436187	Integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide)
AA676470	H.sapiens IAI.3B mRNA
AA443634	Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds
AA664180	Glutathione peroxidase 3 (plasma)
W58658	H.sapiens mRNA for CLPP
H54023	Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds
H73724	Cyclin-dependent kinase 6
T70031	Human neutral amino acid transporter B mRNA, complete cds
AA481758	DNAJ PROTEIN HOMOLOG 1
AA521431	Human profilin mRNA, complete cds
AA446103	ERGIC-53 PROTEIN PRECURSOR
N92646	Immunoglobulin gamma 3 (Gm marker)
AA453789	Protein-tyrosine kinase 7
AA425299	Homo sapiens ezrin-radixin-moesin binding phosphoprotein-50 mRNA, complete cds
AA868929	Troponin T1, skeletal, slow
R60019	Homolog 2 of Drosophila large discs
AA857343	Human putative RNA binding protein (RBP56) mRNA, complete cds
AA481438	Complement component 1 inhibitor (angioedema, hereditary)
AA399674	Human small proline rich protein (sprl1) mRNA, clone 1292
T98887	Glucose-6-phosphatase
AA676404	Peptidylprolyl isomerase C (cyclophilin C)
H15747	Human HU-K4 mRNA, complete cds
H16958	Human glyceraldehyde 3-phosphate dehydrogenase mRNA
AA936783	Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit
AA884709	Cytochrome P450 11 beta
H24688	Human SWI/SNF complex 170 KDa subunit (BAF170) mRNA, complete cds
AA884403	Human cardiotrophin-1 (CTF1) mRNA, complete cds
AA404619	5' nucleotidase (CD73)
AA598611	IMMEDIATE-EARLY RESPONSE PROTEIN NOT
H72875	GATA-binding protein 3
H63361	Eukaryotic translation initiation factor 2B (eIF-2B) alpha subunit
R39221	Human MAP kinase mRNA, complete cds
R02346	U1 snRNP 70K protein
R51835	unknown EST
R33031	H.sapiens mRNA for sigma 3B protein
AA412053	CD9 antigen
AA001897	Erythroid alpha-spectrin

W81191	Homo sapiens nucleolar autoantigen No55 mRNA, complete cds
AA430552	Homo sapiens proline-rich Gla protein 2 (PRGP2) mRNA, complete cds
AA394130	Human transducin-like protein mRNA, complete cds
N92864	Human cleavage and polyadenylation specificity factor mRNA, complete cds
AA457123	VALYL-TRNA SYNTHETASE
R43320	Human guanine nucleotide-binding regulatory protein (Go-alpha) gene
AA670430	Glutamate receptor, metabotropic 3
H65066	Visinin-like 1
AA458785	GUANYLATE CYCLASE SOLUBLE, BETA-1 CHAIN
AA485871	H.sapiens mRNA for myosin-I beta
T39411	Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds
R00855	Homo sapiens 59 protein mRNA, 3' end
H98666	Metallopeptidase 1 (33 kD)
H72028	GELSOLIN PRECURSOR, PLASMA
AA679177	Human follistatin-related protein precursor mRNA, complete cds
N21576	Human mitochondrial 1,25-dihydroxyvitamin D3 24-hydroxylase mRNA, complete cds
AA007419	Human RGP4 mRNA, complete cds
T49657	Homo sapiens TWIK-related acid-sensitive K ⁺ channel (TASK) mRNA, complete cds
N38959	Homo sapiens chaperonin containing t-complex polypeptide 1, beta subunit (Cctb) mRNA, complete cds
R51912	Human somatostatin I gene and flanks
H90415	Breast cancer 1, early onset
H41489	Adaptin, beta 1 (beta prime)
H15456	CALPAIN 1, LARGE
W45415	ELASTASE IIIB PRECURSOR
AA447751	Tyrosine hydroxylase
AA487486	Cyclin D1 (PRAD1; parathyroid adenomatosis 1)
R56604	Cholinergic receptor, nicotinic, alpha polypeptide 4
T65772	pulmonary surfactant protein (SP5)
H15085	ADP-ribosylation factor 4-like
R61295	Human ADP/ATP translocase mRNA, 3' end, clone pHAT8
T61256	H.sapiens KHK mRNA for ketohexokinase, clone pHKHK3a
AA405731	Phosphoenolpyruvate carboxykinase 1 (soluble)
T71879	Complement component C2
R59927	Human mRNA for cytochrome c oxidase subunit VIc
AA496780	Human small GTP binding protein Rab7 mRNA, complete cds
AA176688	Human mRNA for lysosomal sialoglycoprotein, complete cds
AA436163	Homo sapiens Pig12 (PIG12) mRNA, complete cds
AA428778	Human placenta LERK-2 (EPLG2) mRNA, complete cds
AA463225	Bone morphogenetic protein 4
AA485426	Interferon (alpha, beta and omega) receptor 2
W47485	Human sigma receptor mRNA, complete cds
H84982	Human checkpoint suppressor 1 mRNA, complete cds
AA504615	Homo sapiens mRNA for CAB1, complete cds
H94487	Cathepsin E
AA448959	Homo sapiens NADH:ubiquinone oxidoreductase 15 kDa IP subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds
AA070358	Transketolase (Wernicke-Korsakoff syndrome)
AA453401	Human PH-20 homolog (LUCA2) mRNA, partial cds
N66737	Collagen, type II, alpha 1 (primary osteoarthritis, spondyloepiphyseal dysplasia, congenital)
AA666180	Human v-erbA related ear-2 gene
AA857131	Human Tat-SF1 mRNA, complete cds
AA479102	Protein kinase C, beta 1

AA456077	Homo sapiens mRNA for p27, complete cds
R87497	H.sapiens mRNA for 2.19 gene
AA718910	Human tax1-binding protein TXBP181 mRNA, complete cds
AA406269	Nuclear factor I/X (CCAAT-binding transcription factor)
N74623	Insulin-like growth factor 2 (somatomedin A)
H99364	Human chloride channel protein (CLCN7) mRNA, partial cds
AA447684	Small proline-rich protein 1B (cornifin)
AA282301	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
H99588	Human lymphoid nuclear protein (LAF-4) mRNA, complete cds
N53512	Homo sapiens alpha 2 delta calcium channel subunit isoform I mRNA, complete cds
AA683321	Homo sapiens PAR-5 mRNA, probable 5' end
AA608557	Damage-specific DNA binding protein 1 (127 kD)
AA757764	Homo sapiens mRNA for DNA-binding protein, complete cds
AA406064	Homo sapiens testis-specific Basic Protein Y 1 (BPY1) mRNA, complete cds
N54596	Human Krueppel-related zinc finger protein (H-plk) mRNA, complete cds
AA481988	Transcription factor 7 (T-cell specific)
N62394	Gap junction protein, beta 1, 32kD (connexin 32, Charcot-Marie-Tooth neuropathy, X-linked)
N26148	Zinc finger protein 148 (pHZ-52)
AA496678	B-cell CLL/lymphoma 3
AA400973	NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR
AA497027	Human mRNA, clone HH109 (screened by the monoclonal antibody of insulin receptor substrate-1 (IRS-1))
N64508	Homo sapiens podocalyxin-like protein mRNA, complete cds
AA033564	H.sapiens mRNA for DGCR6 protein
AA446108	Endoglin (Osler-Rendu-Weber syndrome 1)
AA159577	Mucin 5, subtype B, tracheobronchial
R36958	unknown EST
AA629808	Ribosomal protein L6
AA482067	Human tazarotene-induced gene 2 (TIG2) mRNA, complete cds
AA669314	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit
AA775241	Aldolase A
R73584	Homo sapiens hydroxysteroid sulfotransferase SULT2B1a (HSST2) mRNA, complete cds
H28984	PHOSPHATIDYL SERINE SYNTHASE I
R44202	Homo sapiens catechol-O-methyltransferase (COMT) mRNA, complete cds
W70051	H.sapiens mRNA for M-phase phosphoprotein, mpp9
AA401972	Human RalGDS-like 2 (RGL2) mRNA, partial cds
AA236164	CATHEPSIN S PRECURSOR
R22412	Platelet/endothelial cell adhesion molecule (CD31 antigen)
AA424804	MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 1
AA669443	Eukaryotic translation initiation factor 5 (eIF5)
N69689	RAS-RELATED PROTEIN RAB-1A
H24316	AQUAPORIN-CHIP
AA074224	Recoverin
R36571	Human U1 snRNP-specific protein A gene
AA056465	Human 54 kDa protein mRNA, complete cds
AA633811	H.sapiens E4BP4 gene
AA457155	Human zinc-finger protein C2H2-150 mRNA, complete cds
AA459104	60S RIBOSOMAL PROTEIN L13
R40212	Human coatamer protein (HEPCOP) mRNA, complete cds
AA086476	Adenosine monophosphate deaminase 1 (isoform M)
AA663310	Thymidylate synthase
AA455640	Homo sapiens signalosome subunit 3 (Sgn3) mRNA, complete cds
AA496879	Human (clone E5.1) RNA-binding protein mRNA, complete cds

AA085749	Homo sapiens mRNA for ATP binding protein, complete cds
AA425755	Homo sapiens mRNA for leukemia associated gene 1
N52350	H.sapiens mRNA for protein-tyrosine-phosphatase (tissue type: testis)
AA630104	Lipase A, lysosomal acid, cholesterol esterase (Wolman disease)
AA454854	ALPHA-AMYLASE 2B PRECURSOR
W73406	DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT
R12802	Human cytochrome bc-1 complex core protein II mRNA, complete cds
AA465355	Homo sapiens mRNA for U3 snoRNP associated 55 kDa protein
AA829383	DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3
AA629189	Keratin 4
AA430512	Homo sapiens cytoplasmic antiproteinase 3 (CAP3) mRNA, complete cds
AA456439	Human homozygous deletion target in pancreatic carcinoma (DPC4) mRNA, complete cds
H27864	SECRETOGRANIN II PRECURSOR
AA644657	MHC class I protein HLA-A (HLA-A28,-B40, -Cw3)
R40460	Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds
W96058	Human hnRNP H mRNA, complete cds
T72202	Human transcription factor IL-4 Stat mRNA, complete cds
AA598794	Connective tissue growth factor
AA599178	Ribosomal protein L27a
R88247	Adrenergic, beta, receptor kinase 1
T98612	Alpha-1 type 3 collagen
AA454856	Phospholipid hydroperoxide glutathione peroxidase
N67048	Type 3 iodothyronine deiodinase
AA778675	Homo sapiens mRNA for calmegin, complete cds
H51117	Human calmodulin dependent phosphodiesterase PDE1B1 mRNA, complete cds
N36174	5-HYDROXYTRYPTAMINE 2B RECEPTOR
AA777187	Homo sapiens Cyr61 mRNA, complete cds
R09561	Decay accelerating factor for complement (CD55, Cromer blood group system)
R16849	Human HsPex13p mRNA, complete cds
AA884167	ANNEXIN XIII
AA136983	Cadherin 11 (OB-cadherin)
AA488622	Human signal transducing adaptor molecule STAM mRNA, complete cds
AA699427	Fructose-bisphosphatase 1
AA490459	Transcobalamin II
AA626787	Human ras-related C3 botulinum toxin substrate (rac) mRNA, complete cds
N62179	Human methylmalonate semialdehyde dehydrogenase gene, complete cds
N27190	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L3
AA441895	Human glutathione-S-transferase homolog mRNA, complete cds
AA463924	FACTOR VIII INTRON 22 PROTEIN
N78843	Homo sapiens cyclophilin-33A (CYP-33) mRNA, complete cds
AA629719	Cytochrome c oxidase VIIc subunit
AA464755	Ankyrin 1, erythrocytic
AA459351	H.sapiens sds22-like mRNA
AA488346	MYOSIN LIGHT CHAIN ALKALI, SMOOTH-MUSCLE ISOFORM
AA427899	Human mRNA fragment encoding beta-tubulin. (from clone D-beta-1)
AA453813	H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sialyltransferase
AA397824	Dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)
AA633901	Transforming growth factor, beta-induced, 68kD
AA181334	Troponin I (skeletal fast)
AA292410	Clusterin (complement lysis inhibitor; testosterone-repressed prostate message 2; apolipoprotein J)
AA253434	HEAT SHOCK FACTOR PROTEIN 2
AA455056	H.sapiens mRNA for MAP kinase activated protein kinase

R55188	Human pre-T/NK cell associated protein (3B3) mRNA, 3' end
AA465723	Homo sapiens mRNA for protein phosphatase 2C gamma
N49856	SODIUM- AND CHLORIDE-DEPENDENT BETAINE TRANSPORTER
AA455272	H.sapiens mRNA for ITBA1 protein
AA459292	CDC28 protein kinase 1
AA878561	Ubiquitin A-52 residue ribosomal protein fusion product 1
AA772066	Human phosphatidylinositol (4,5)bisphosphate 5-phosphatase homolog mRNA, partial cds
N78621	H.sapiens mRNA for gamma-adaptin
AA291490	H.sapiens mRNA for processing a-glucosidase I
N46828	Homo sapiens mRNA for inositol 1,4,5-trisphosphate 3-kinase isoenzyme, partial cds
AA150487	Alkaline phosphatase, placental (Regan isozyme)
AA282537	MYOCYTE-SPECIFIC ENHANCER FACTOR 2
AA707922	Human mRNA for cone-specific cGMP phosphodiesterase gamma subunit, complete cds
AA443638	Homo sapiens breast cancer-specific protein 1 (BCSG1) mRNA, complete cds
W73892	Human putative tumor suppressor (LUCA15) mRNA, complete cds
N70734	Troponin T2 (cardiac)
H57136	Human phospholemman chloride channel mRNA, complete cds
AA709414	Nidogen (enactin)
W65461	Human protein tyrosine phosphatase mRNA, complete cds
AA436564	Human cellular proto-oncogene (c-mer) mRNA, complete cds
AA029042	Human hSIAH2 mRNA, complete cds
AA427725	Homo sapiens carboxypeptidase Z precursor, mRNA, complete cds
N51280	ADP-ribosylation factor like 1
AA281347	H.sapiens mRNA for MHC class I promoter binding protein
AA402960	Human HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds
N98485	Human forkhead protein FREAC-2 mRNA, partial cds
AA490209	H.sapiens mRNA for Sop2p-like protein
W61361	Homo sapiens cytoplasmic antiproteinase 2 (CAP2) mRNA, complete cds
N51018	Biglycan
AA455281	DEFENDER AGAINST CELL DEATH 1
W69471	V-ski avian sarcoma viral oncogene homolog
AA486321	Vimentin
AA458982	Solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na ⁺ /H ⁺ , amiloride sensitive)
AA442095	NEDD-4 PROTEIN
N99003	Active BCR-related gene
AA609284	Homo sapiens mRNA for Eph-family protein, complete cds
AA195036	Human Ro/SSA ribonucleoprotein homolog (RoRet) mRNA, complete cds
AA478268	Human CtBP mRNA, complete cds
AA608583	Homo sapiens mRNA for OTK27, complete cds
AA486435	Homo sapiens mRNA for CDEP, complete cds
AA505045	Human L2-9 transcript of unrearranged immunoglobulin V(H)5 pseudogene
AA487893	TUMOR-ASSOCIATED ANTIGEN L6
AA292226	Homo sapiens creatine transporter mRNA, complete cds
H87106	Homo sapiens T245 protein (T245) mRNA, complete cds
W96450	Human putative tRNA synthetase-like protein mRNA, complete cds
N33331	Human peroxisome proliferator activated receptor mRNA, complete cds
AA405800	Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
T51539	Macrophage stimulating 1 (hepatocyte growth factor-like)
N59764	Human guanosine 5'-monophosphate synthase mRNA, complete cds
AA521346	H.sapiens mRNA for Ndr protein kinase

AA428551	Homo sapiens SOX22 protein (SOX22) mRNA, complete cds
AA489383	Bone morphogenetic protein 2
AA490172	Collagen, type I, alpha-2
AA504477	Human cytoskeleton associated protein (CG22) mRNA, complete cds

List of Table III related sequences:

Accession_	NAME	Gene
mrgd		
M98539	Human prostaglandin D2 synthase gene, exon 7	
AB004922	Homo sapiens gene for Smad 3, exon 1, partial sequence	
AB006000	Homo sapiens mRNA for chondromodulin-1 precursor, complete cds	
AB017364	Homo sapiens mRNA for frizzled-2, complete cds	Ribosomal protein L27a
AB020236	Homo sapiens gene for ribosomal protein L27A, complete cds	Ribosomal protein L6
AB042820	Homo sapiens RPL6 gene for ribosomal protein L6, complete cds	
AB043547	Homo sapiens gene for SMAD4, partial cds	
AB080265	Homo sapiens CYP2J2 mRNA for cytochrome P450 2J2, complete cds	Cytochrome P450, subfamily IIJ (arachidonic acid epoxidase) polypeptide 2
AF000979	Homo sapiens testis-specific Basic Protein Y 1 (BPY1) mRNA, complete cds	Homo sapiens testis-specific Basic Protein Y 1 (BPY1) mRNA, complete cds
AF001450	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 7 and complete cds	
AF004231	Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds	Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds
AF009801	Homo sapiens homeodomain protein (BAPX1) mRNA, complete cds	
AF010126	Homo sapiens breast cancer-specific protein 1 (BCSG1) mRNA, complete cds	Homo sapiens breast cancer-specific protein 1 (BCSG1) mRNA, complete cds
AF010316	Homo sapiens Pig12 (PIG12) mRNA, complete cds	Homo sapiens Pig12 (PIG12) mRNA, complete cds
AF013591	Homo sapiens homolog of the Aspergillus nidulans sudD gene product mRNA, complete cds	Homo sapiens homolog of the Aspergillus nidulans sudD gene product mRNA, complete cds
AF037204	Homo sapiens RING zinc finger protein (RZF) mRNA, complete cds	
AF043339	Homo sapiens macrophage inflammatory protein 1 alpha (MIP1a) mRNA, partial cds	
AF049656	Homo sapiens inducible nitric oxide synthase (iNOS) mRNA, complete cds	
AF072872	Homo sapiens frizzled 1 mRNA, complete cds	
AF188285	Homo sapiens bone morphogenetic protein 9 (BMP9) mRNA, complete cds	
AF189279	Homo sapiens group IIE secretory phospholipase A2 mRNA, complete cds	
AF248634	Homo sapiens syndecan 3 (SDC3) mRNA, complete cds	
AF504431	Homo sapiens hypoxia-inducible factor 1 alpha subunit (HIF1A) mRNA, complete cds	

AF339054	Homo sapiens BCL2-associated X protein (BAX) gene, exons 1, 2 and partial cds	
AF348700	Homo sapiens ubiquitin A-52 residue ribosomal protein fusion product 1 (UBA52), mRNA, complete cds	Ubiquitin A-52 residue ribosomal protein fusion product 1
AF395008	Homo sapiens interleukin 4 (IL4) gene, complete cds	
AF405705	Homo sapiens matrix metalloproteinase 3 (stromelysin 1, progelatinase) (MMP3) gene, complete cds	
AF411526	Homo sapiens nerve growth factor beta (NGFB) mRNA, complete cds	Nerve growth factor beta
AF469046	Homo sapiens macrophage migration inhibitory factor (MIF) mRNA, complete cds	
AF477981	Homo sapiens osterix mRNA, complete cds	
AJ279016	Homo sapiens mRNA for chondrocyte expressed protein 68 kDa (CEP-68 gene)	
AY043326	Homo sapiens keratin 4 (KRT4) gene, complete cds	Keratin 4
AY044847	Homo sapiens aggrecanase 1 (ADAMTS4) gene, complete cds	
D13748	Human mRNA for eukaryotic initiation factor 4A1	Human mRNA for eukaryotic initiation factor 4A1
D38255	Homo sapiens mRNA for CAB1, complete cds	Homo sapiens mRNA for CAB1, complete cds
D45399	Human mRNA for cone-specific cGMP phosphodiesterase gamma subunit, complete cds	Human mRNA for cone-specific cGMP phosphodiesterase gamma subunit, complete cds
D49738	Human cytoskeleton associated protein (CG22) mRNA, complete cds	Human cytoskeleton associated protein (CG22) mRNA, complete cds
D49835	Homo sapiens mRNA for DNA-binding protein, complete cds	Homo sapiens mRNA for DNA-binding protein, complete cds
D90040	Human mRNA for arylamine N-acetyltransferase (EC 2.3.1.5)	ARYLAMINE N-ACETYLTRANSFERASE, MONOMORPHIC
J00306	Human somatostatin I gene and flanks	Human somatostatin I gene and flanks
J03191	Human profilin mRNA, complete cds	Human profilin mRNA, complete cds
J03592	Human ADP/ATP translocase mRNA, 3' end, clone pHAT8	Human ADP/ATP translocase mRNA, 3' end, clone pHAT8
J04111	Human c-jun proto oncogene (JUN), complete cds, clone hCJ-1	
J04177	Human alpha-1 type XI collagen (COL11A1) mRNA, complete cds	
J04973	Human cytochrome bc-1 complex core protein II mRNA, complete cds	Human cytochrome bc-1 complex core protein II mRNA, complete cds
J05036	Human cathepsin E mRNA, complete cds	Cathepsin E
K00065	Human superoxide dismutase (SOD-1) mRNA, complete cds	Human superoxide dismutase (SOD-1) mRNA, complete cds
K00650	Human fos proto-oncogene (c-fos), complete cds	
L05095	Homo sapiens ribosomal protein L30 mRNA, complete cds	60S RIBOSOMAL PROTEIN L30
L08895	Homo sapiens MADS/MEF2-family transcription factor (MEF2C) mRNA, complete cds	
L10347	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds	
L11566	Homo sapiens ribosomal protein L18 (RPL18) mRNA, complete cds	60S RIBOSOMAL PROTEIN L18

L13286	Human mitochondrial 1,25-dihydroxyvitamin D3 24-hydroxylase mRNA, complete cds	Human mitochondrial 1,25-dihydroxyvitamin D3 24-hydroxylase mRNA, complete cds
L13463	Human helix-loop-helix basic phosphoprotein (GOS8) mRNA, complete cds	
L13616	Human focal adhesion kinase (FAK) mRNA, complete cds	
L13720	Homo sapiens growth-arrest-specific protein (gas) mRNA, complete cds	Homo sapiens growth-arrest-specific protein (gas) mRNA, complete cds
L22009	Human hnRNP H mRNA, complete cds	Human hnRNP H mRNA, complete cds
L28997	Homo sapiens ARL1 mRNA, complete cds	ADP-ribosylation factor like 1
L31409	Homo sapiens creatine transporter mRNA, complete cds	Homo sapiens creatine transporter mRNA, complete cds
L33930	Homo sapiens CD24 signal transducer mRNA, complete cds and 3' region	
L34059	Homo sapiens cadherin-4 mRNA, complete cds	
L41162	Homo sapiens collagen alpha 3 type IX (COL9A3) mRNA, complete cds	
L47647	Homo sapiens creatine kinase B mRNA, complete cds	Creatine kinase B
M13994	Human B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene mRNA encoding bcl-2-alpha protein, complete cds	bcl-2-alpha protein, complete cds
M14144	Human vimentin gene, complete cds	Vimentin
M14631	Human guanine nucleotide-binding protein G-s, alpha subunit mRNA, partial cds	Human guanine nucleotide-binding protein G-s, alpha subunit mRNA, partial cds
M16652	Human pancreatic elastase IIA mRNA, complete cds	Elastase 1, pancreatic (elastase IIA)
M20137	Human interleukin 3 (IL-3) mRNA, complete cds, clone pcD-SR-alpha	
M22636	Human U1 small nuclear ribonucleoprotein 70 kd protein mRNA, complete cds	U1 snRNP 70K protein
M37825	Human fibroblast growth factor-5 (FGF-5) mRNA, complete cds	
M57293	Human parathyroid hormone-related peptide (PTHrP) gene, exons 1A, 1B, 1C, and 2	
M58458	Human ribosomal protein S4 (RPS4X) isoform mRNA, complete cds	Ribosomal protein S4, X-linked
M58525	Homo sapiens catechol-O-methyltransferase (COMT) mRNA, complete cds	Homo sapiens catechol-O-methyltransferase (COMT) mRNA, complete cds
M58549	Human matrix Gla protein (MGP) mRNA, complete cds	
M61877	Human erythroid alpha-spectrin (SPTA1) mRNA, complete cds	Erythroid alpha-spectrin
M62402	Human insulin-like growth factor binding protein 6 (IGFBP6) mRNA, complete cds	Insulin-like growth factor binding protein 6
M65062	Human insulin-like growth factor binding protein 5 (IGFBP-5) mRNA, complete cds	
M65217	Human heat shock factor 2 (HSF2) mRNA, complete cds	HEAT SHOCK FACTOR PROTEIN 2
M76701	Homo sapiens zinc finger protein 35 (ZNF35) gene, exon 1	
M77016	Human tropomodulin mRNA, complete cds	Tropomodulin

M81768	Human Na/H antiporter (APNH1) mRNA, complete cds	Human Na/H antiporter (APNH1) mRNA, complete cds
M84489	Human extracellular signal-regulated kinase 2 mRNA, complete cds	
M84721	Human AMP deaminase (AMPD3) mRNA, complete cds	Adenosine monophosphate deaminase (isoform E)
M87842	Human S-lac lectin L-14-II (LGALS2) mRNA, complete cds	GALECTIN-2
M92934	Human connective tissue growth factor, complete cds	Connective tissue growth factor
M95610	Human alpha 2 type IX collagen (COL9A2) mRNA, partial cds	
M96684	H.sapiens Pur (pur-alpha) mRNA, complete cds	H.sapiens Pur (pur-alpha) mRNA, complete cds
M97676	Homo sapiens (region 7) homeobox protein (HOX7) mRNA, complete cds	
NM_000194	Homo sapiens hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	(HPRT1), mRNA
NM_000213	Homo sapiens integrin, beta 4 (ITGB4), mRNA	
NM_000221	Homo sapiens ketohexokinase (fructokinase) (KHK), transcript variant a, mRNA	H.sapiens KHK mRNA for ketohexokinase, clone pHKHK3a
NM_000235	Homo sapiens lipase A, lysosomal acid, cholesterol esterase (Wolman disease) (LIPA), mRNA	Lipase A, lysosomal acid, cholesterol esterase (Wolman disease)
NM_000358	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA	Transforming growth factor, beta-induced, 68kD
NM_000364	Homo sapiens troponin T2, cardiac (TNNT2), mRNA	Troponin T2 (cardiac)
NM_000537	Homo sapiens renin (REN), mRNA	RENIN PRECURSOR, RENAL
NM_000574	Homo sapiens decay accelerating factor for complement (CD55, Cromer blood group system) (DAF), mRNA	Decay accelerating factor for complement (CD55, Cromer blood group system)
NM_000600	Homo sapiens interleukin 6 (interferon, beta 2) (IL6), mRNA	
NM_000618	Homo sapiens insulin-like growth factor 1 (somatomedia C) (IGF1), mRNA	
NM_000632	Homo sapiens integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide) (ITGAM), mRNA	Integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide)
NM_000711	Homo sapiens bone gamma-carboxyglutamate (gla) protein (osteocalcin) (BGLAP), mRNA	Prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
NM_000962	Homo sapiens prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) (PTGS1), transcript variant 1, mRNA	60S RIBOSOMAL PROTEIN L13
NM_000977	Homo sapiens ribosomal protein L13 (RPL13), transcript variant 1, mRNA	Ribosomal protein L35a
NM_000996	Homo sapiens ribosomal protein L35a (RPL35A), mRNA	40S RIBOSOMAL PROTEIN S8
NM_001012	Homo sapiens ribosomal protein S8 (RPS8), mRNA	40S RIBOSOMAL PROTEIN S23
NM_001025	Homo sapiens ribosomal protein S23 (RPS23), mRNA	Transketolase (Wernicke-Korsakoff syndrome)
NM_001064	Homo sapiens transketolase (Wernicke-Korsakoff syndrome) (TKT), mRNA	Adaptin, beta 1 (beta prime)
NM_001127	Homo sapiens adaptor-related protein complex 1, beta 1 subunit	

NM_001200	Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA	AP1B1), mRNA
NM_001229	Homo sapiens caspase 9, apoptosis-related cysteine protease (CASP9), transcript variant alpha, mRNA	Bone morphogenetic protein 2
NM_001511	Homo sapiens GRO1 oncogene (melanoma growth stimulating activity, alpha) (GRO1), mRNA	Transcript variant alpha, mRNA
NM_001565	Homo sapiens small inducible cytokine subfamily B (Cys-X-Cys), member 10 (SCYB10), mRNA	Interferon (gamma)-induced cell line; protein 10 from
NM_001632	Homo sapiens alkaline phosphatase, placental (Regan isozyme) (ALPP), mRNA	Alkaline phosphatase, placental (Regan isozyme)
NM_001687	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), mRNA	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit
NM_001718	Homo sapiens bone morphogenetic protein 6 (BMP6), mRNA	Calcium modulating ligand
NM_001745	Homo sapiens calcium modulating ligand (CAMLG), mRNA	Transcript variant 1, mRNA
NM_001797	Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 1, mRNA	Transcript variant 1, mRNA
NM_001844	Homo sapiens collagen, type II, alpha 1 (primary osteoarthritis, spondyloepiphyseal dysplasia, congenital) (COL2A1), transcript variant 1, mRNA	Transcript variant 1, mRNA
NM_001912	Homo sapiens cathepsin L (CTSL), mRNA	
NM_001969	Homo sapiens eukaryotic translation initiation factor 5 (EIF5), mRNA	Eukaryotic translation initiation factor 5 (eIF5)
NM_002073	Homo sapiens guanine nucleotide binding protein (G protein), alpha z polypeptide (GNAZ), mRNA	Guanine nucleotide binding protein (G protein), alpha z polypeptide
NM_002094	Homo sapiens G1 to S phase transition 1 (GSPT1), mRNA	G1 to S phase transition 1
NM_002160	Homo sapiens hexabrachion (tenascin C, cytotoxic) (HXB), mRNA	
NM_002211	Homo sapiens integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), mRNA	
NM_002379	Homo sapiens matrilin 1, cartilage matrix protein (MATN1), mRNA	
NM_002381	Homo sapiens matrilin 3 (MATN3) precursor, mRNA	
NM_002421	Homo sapiens matrix metalloproteinase 1 (interstitial collagenase) (MMP1), mRNA	
NM_002424	Homo sapiens matrix metalloproteinase 8 (neutrophil collagenase) (MMP8), mRNA	
NM_002427	Homo sapiens matrix metalloproteinase 13 (collagenase 3) (MMP13), mRNA	
NM_002591	Homo sapiens phosphoenolpyruvate carboxykinase 1 (soluble) (PCK1), mRNA	Phosphoenolpyruvate carboxykinase 1 (soluble)
NM_002619	Homo sapiens platelet factor 4 (PF4), mRNA	Platelet factor 4
NM_002722	Homo sapiens pancreatic polypeptide (PPY), mRNA	
NM_002738	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA	Protein kinase C, beta 1
NM_002903	Homo sapiens recoverin (RCV1), mRNA	Recoverin

NM_003036	Homo sapiens v-ski sarcoma viral oncogene homolog (avian) (SKI), mRNA	V-ski avian sarcoma viral oncogene homolog
NM_003282	Homo sapiens troponin I, skeletal, fast (TNNI2), mRNA	Troponin I (skeletal fast)
NM_003385	Homo sapiens visinin-like 1 (VSNL1),	Visinin-like 1
NM_003395	Homo sapiens wingless-type MMTV integration site family, member 14 (WNT14), mRNA	WNT14, mRNA
NM_004613	Homo sapiens transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM2), mRNA	TGM2, mRNA
NM_004832	Homo sapiens glutathione-S-transferase like; glutathione transferase omega (GSTT1p28), mRNA	Human glutathione-S-transferase homolog mRNA, complete cds
NM_004994	Homo sapiens matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase) (MMP9), mRNA	MMP9, mRNA
NM_004995	Homo sapiens matrix metalloproteinase 14 (membrane-inserted) (MMP14), mRNA	MMP14, mRNA
NM_005038	Homo sapiens peptidylprolyl isomerase D (cyclophilin D) (PPID), mRNA	40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE
NM_005186	Homo sapiens calpain 1, (mu/I) large subunit (CAPN1), mRNA	CALPAIN 1, LARGE
NM_005346	Homo sapiens heat shock 70kD protein 1B (HSPA1B), mRNA	HEAT SHOCK 70 KD PROTEIN 1
NM_005438	Homo sapiens FOS-like antigen 1 (FOSL1), mRNA	
NM_005506	Homo sapiens CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein II) (CD36L2), mRNA	CD36L2, mRNA
NM_006289	Homo sapiens talin 1 (TLN1), mRNA	
NM_006988	Homo sapiens a disintegrin-like and metalloprotease (repolyisin type) with thrombospondin type 1 motif, 1 (ADAMTS1), mRNA	ADAMTS1, mRNA
NM_007306	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA	Breast cancer 1, early onset
NM_007352	Homo sapiens elastase 3B, pancreatic (ELA3B), Mma	ELASTASE IIIB PRECURSOR
NM_014000	Homo sapiens vinculin (VCL), transcript variant meta-VCL, mRNA	
NM_014470	Homo sapiens GTP-binding protein (RHO6), mRNA	
NM_018952	Homo sapiens homeo box B6 (HOXB6), mRNA	
NM_021019	Homo sapiens myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 1, mRNA	MYOSIN LIGHT CHAIN ALKALI, SMOOTH-MUSCLE ISOFORM
NM_033150	Homo sapiens collagen, type II, alpha 1 (primary osteoarthritis, spondyloepiphyseal dysplasia, congenital) (COL2A1), transcript variant 2, mRNA	COL2A1, transcript variant 2, mRNA
NM_053056	Homo sapiens cyclin D1 (PRAD1: parathyroid adenomatosis 1) (CCND1), mRNA	Cyclin D1 (PRAD1; parathyroid adenomatosis 1)
NM_080682	Homo sapiens vascular cell adhesion molecule 1 (VCAM1), transcript variant 2, mRNA	VCAM1, transcript variant 2, mRNA
S79854	Homo sapiens type 3 iodothyronine deiodinase mRNA, complete cds	Type 3 iodothyronine deiodinase
S83308	SOX5=Sox5-related HMG box gene [alternatively spliced] [human, testis, mRNA, 1473 nt]	
U07424	Human putative tRNA synthetase-like protein mRNA, complete cds	Human putative tRNA synthetase-like protein mRNA, complete cds

U07620	Human MAP kinase mRNA, complete cds	Human MAP kinase mRNA, complete cds
U08023	Human cellular proto-oncogene (c-mer) mRNA, complete cds	Human cellular proto-oncogene (c-mer) mRNA, complete cds
U09303	Human T cell leukemia LERK-2 (EPLG2) mRNA, complete cds	
U09577	Homo sapiens lysosomal hyaluronidase (LUCA2/HYAL2) mRNA, complete cds	Human PH-20 homolog (LUCA2) mRNA, partial cds
U09825	Human acid finger protein mRNA, complete cds	Acid finger protein ZNF173
U13261	Homo sapiens eIF-2-associated p67 homolog mRNA, complete cds	Human eIF-2-associated p67 homolog mRNA, complete cds
U13660	Human cartilage-derived morphogenetic protein 1 (CDMP-1) mRNA, complete cds	
U13991	Human TATA-binding protein associated factor 30 kDa subunit (tafl130) mRNA, complete cds	Human TATA-binding protein associated factor 30 kDa subunit (tafl130) mRNA, complete cds
U14966	Human ribosomal protein L5 mRNA, complete cds	Ribosomal protein L5
U14971	Human ribosomal protein S9 mRNA, complete cds	
U15085	Human HLA-DMB mRNA, complete cds	Major histocompatibility complex, class II, DM beta
U16031	Human transcription factor IL-4 Stat mRNA, complete cds	Human transcription factor IL-4 Stat mRNA, complete cds
U16261	Human MDA-7 (mda-7) mRNA, complete cds	
U18299	Human damage-specific DNA binding protein DDBa p127 subunit (DDB1) mRNA, complete cds	Damage-specific DNA binding protein 1 (127 kD)
U20980	Human chromatin assembly factor-I p60 subunit mRNA, complete cds	Human chromatin assembly factor-I p60 subunit mRNA, complete cds
U22409	Human parathyroid hormone/PTH-related peptide receptor (PTH/PTHrP) gene, exon 14 and complete cds	Human eukaryotic initiation factor 2B-epsilon mRNA, partial cds
U23028	Human eukaryotic initiation factor 2B-epsilon mRNA, partial cds	
U23946	Human putative tumor suppressor (LUCA15) mRNA, complete cds	Human putative tumor suppressor (LUCA15) mRNA, complete cds
U24152	Human p21-activated protein kinase (Pak1) gene, complete cds	Human protein kinase PAK1 mRNA, complete cds
U25789	Human ribosomal protein L21 mRNA, complete cds	Ribosomal protein L21
U27699	Human pephBGT-1 betaine-GABA transporter mRNA, complete cds	SODIUM- AND CHLORIDE-DEPENDENT BETAINES TRANSPORTER
U31202	Human noggin (NOGGIN) gene, complete cds, (NOG)	
U32169	Human pro-a2 chain of collagen type XI (COL11A2) gene, complete cds	
U32907	Human p37NB mRNA, complete cds	Human p37NB mRNA, complete cds
U33822	Human tax1-binding protein TXBP181 mRNA, complete cds	Human tax1-binding protein TXBP181 mRNA, complete cds
U37012	Human cleavage and polyadenylation specificity factor mRNA, complete cds	Human cleavage and polyadenylation specificity factor mRNA, complete cds
U38864	Human zinc-finger protein C2H2-150 mRNA, complete cds	Human zinc-finger protein C2H2-150 mRNA, complete cds

U40373	Human cell surface glycoprotein CD44 mRNA, complete cds	
U41517	Human channel-like integral membrane protein (AQP-1) mRNA, clone AQP-1-1656, complete cds	AQUAPORIN-CHIP
U43148	Human patched homolog (PTC) mRNA, complete cds	
U43747	Human frataxin (FRDA) mRNA, complete cds	Friedreich ataxia
U43842	Homo sapiens bone morphogenetic protein-4 (hBMP-4) gene, complete cds	Bone morphogenetic protein 4
U45975	Human phosphatidylinositol (4,5)bisphosphate 5-phosphatase homolog mRNA, partial cds	Human phosphatidylinositol (4,5)bisphosphate 5-phosphatase homolog mRNA, partial cds
U53204	Human plectin (PLEC1) mRNA, complete cds	Human plectin (PLEC1) mRNA, complete cds
U53347	Human neutral amino acid transporter B mRNA, complete cds	Human neutral amino acid transporter B mRNA, complete cds
U59289	Human H-cadherin mRNA, complete cds	
U59423	Human Smad1 mRNA, complete cds	
U63717	Homo sapiens osteoclast stimulating factor mRNA, complete cds	Human osteoclast stimulating factor mRNA, complete cds
U68723	Human checkpoint suppressor 1 mRNA, complete cds	
U70312	Homo sapiens integrin binding protein Del-1 (Del1) mRNA, complete cds	
U72245	Human phospholemman chloride channel mRNA, complete cds	Human phospholemman chloride channel mRNA, complete cds
U75283	Human sigma receptor mRNA, complete cds	
U76992	Human Tat-SF1 mRNA, complete cds	Human sigma receptor mRNA, complete cds
U80998	Human basic helix-loop-helix DNA binding protein (TWIST) gene, complete cds	Human Tat-SF1 mRNA, complete cds
U83460	Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds	Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds
U90547	Human Ro/SSA ribonucleoprotein homolog (RoRet) mRNA, complete cds	Human Ro/SSA ribonucleoprotein homolog (RoRet) mRNA, complete cds
U92268	Homo sapiens mitogen activated protein kinase p38-2 mRNA, complete cds	
U93181	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
X00129	Human mRNA for retinol binding protein (RBP)	
X00588	Human mRNA for precursor of epidermal growth factor receptor	
X02910	Human gene for tumor necrosis factor (TNF-alpha)	
X03742	Human gene for L apoferritin exons 1 and 2	
X04412	Human mRNA for plasma gelsolin	
X06614	Human mRNA for receptor of retinoic acid	GELSOLIN PRECURSOR, PLASMA Human mRNA for receptor of retinoic acid

X12794	Human v-erbA related ear-2 gene	Human v-erbA related ear-2 gene
X14420	Human mRNA for pro-alpha-1 type 3 collagen	
X51801	Human OP-1 mRNA for osteogenic protein	
X54412	Human mRNA for alpha1(IX) collagen (long form)	
X55654	Homo sapiens mitochondrial coxII mRNA for cytochrome C oxidase II subunit	
X55764	Human mRNA for cytochrome P-450 (11 Beta)	Cytochrome P450 11 beta
X58399	Human L2-9 transcript of unrearranged immunoglobulin V(H)5 pseudogene	Human L2-9 transcript of unrearranged immunoglobulin V(H)5 pseudogene
X58957	H.sapiens alk mRNA for agammaglobulinaemia tyrosine kinase	Agammaglobulinaemia protein-tyrosine kinase atk
X60188	Human ERK1 mRNA for protein serine/threonine kinase	
X60382	H.sapiens COL10A1 gene for collagen (alpha-1 type X)	
X67337	H.sapiens HPBR11-4 mRNA	H.sapiens HPBR11-4 mRNA
X70683	H.sapiens mRNA for SOX-4 protein	
X71661	H.sapiens ERGIC-53 mRNA	ERGIC-53 PROTEIN PRECURSOR
X74795	H.sapiens P1-Cdc46 mRNA	CDC46 HOMOLOG
X76770	H.sapiens PAP mRNA	H.sapiens PAP mRNA
X78712	H.sapiens mRNA for glycerol kinase testis specific 2	Glycerol kinase 2 (testis specific)
X87237	H.sapiens mRNA for processing a-glucosidase I	H.sapiens mRNA for processing a-glucosidase I
X87342	H.sapiens mRNA for human giant larvae homolog	H.sapiens mRNA for human giant larvae homolog
X92475	H.sapiens mRNA for ITBA1 protein	H.sapiens mRNA for ITBA1 protein
X94216	H.sapiens mRNA for VEGF-C protein	
XM_001306	Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 1 (SLC16A1), mRNA	Solute carrier family 16 (monocarboxylic acid transporters), member 1
XM_001316	Homo sapiens adenosine monophosphate deaminase 1 (isoform M) (AMPD1), mRNA	Adenosine monophosphate deaminase 1 (isoform M)
XM_001324	Homo sapiens calponin 3, acidic (CNN3), mRNA	Calponin 3, acidic
XM_001782	Homo sapiens fibromodulin (FMOD), mRNA	
XM_001826	Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA	Alkaline phosphatase, liver/bone/kidney
XM_002321	Homo sapiens glypican 1 (GPC1), mRNA	Glypican 1
XM_003059	Homo sapiens peroxisome proliferative activated receptor, gamma (PPARG), mRNA	
XM_003222	Homo sapiens catenin (cadherin-associated protein), beta 1 (88kD) (CTNNB1), mRNA	
XM_003730	Homo sapiens cytochrome c oxidase subunit VIc (COX7C), mRNA	Cytochrome c oxidase VIc subunit
XM_003752	Homo sapiens interleukin 3 (colony-stimulating factor, multiple) (IL3), mRNA	

XM_003913	Homo sapiens integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) (ITGA2), mRNA	
XM_004063	Homo sapiens early growth response 1 (EGR1), mRNA	
XM_006121	Homo sapiens cathepsin D (lysosomal aspartyl protease) (CTSD), mRNA	
XM_009336	Homo sapiens cartilage oligomeric matrix protein (pseudochondroplasia, epiphyseal dysplasia 1, multiple) (COMP), mRNA	
XM_009915	Homo sapiens leukemia inhibitory factor (cholinergic differentiation factor) (LIF), mRNA	
XM_010702	Homo sapiens cathepsin K (pseudodysostosis) (CTSK), mRNA	
XM_012503	Homo sapiens matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase) (MMP2), mRNA	
XM_012651	Homo sapiens collagen, type I, alpha 1 (COL1A1), mRNA	
XM_015434	Homo sapiens chitinase 3-like 1 (cartilage glycoprotein-39) (CHI3L1), mRNA	
XM_016181	Homo sapiens wingless-type MMTV integration site family, member 5A (WNT5A), mRNA	
XM_017096	Homo sapiens active BCR-related gene (ABR), mRNA	
XM_017384	Homo sapiens matrix metalloproteinase 7 (matrilysin, uterine) (MMP7), mRNA	Matrix metalloproteinase 7 (matrilysin, uterine)
XM_017591	Homo sapiens annexin A6 (ANXA6), mRNA	Annexin VI (p68)
XM_028204	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) (NFKB1), mRNA	
XM_028642	Homo sapiens integrin, alpha 5 (fibronectin receptor, alpha polypeptide) (ITGA5), mRNA	
XM_029245	Homo sapiens collagen, type I, alpha 2 (COL1A2), mRNA	Collagen, type I, alpha-2
XM_029796	Homo sapiens frizzled-related protein (FRZB), mRNA	
XM_031221	Homo sapiens interleukin 1, alpha (IL1A), mRNA	
XM_031288	Homo sapiens aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) (AGC1), mRNA	
XM_031289	Homo sapiens interleukin 8 (IL8), mRNA	
XM_032902	Homo sapiens integrin, alpha 1 (ITGA1), mRNA	
XM_033470	Homo sapiens defender against cell death 1 (DAD1), mRNA	DEFENDER AGAINST CELL DEATH 1
XM_033657	Homo sapiens heparan sulfate proteoglycan 2 (perlecan) (HSPG2), mRNA	
XM_033878	Homo sapiens tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMP1), mRNA	
XM_034023	Homo sapiens regulator of G-protein signalling 4 (RGS4), mRNA	Human RGP4 mRNA, complete cds
XM_034556	Homo sapiens chloride channel 7 (CLCN7), mRNA	
XM_034845	Homo sapiens phosphatase and tensin homolog (mutated in multiple advanced cancers 1) (PTEN), mRNA	Phosphatase and tensin homolog (mutated in multiple advanced cancers 1)
XM_034890	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1), mRNA	
XM_035662	Homo sapiens cathepsin B (CTSB), mRNA	
XM_035842	Homo sapiens small inducible cytokine A5 (RANTES) (SCYA5), mRNA	Small inducible cytokine A5 (RANTES)
XM_036107	Homo sapiens integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1 (mac-1) beta subunit)	

	(ITGB2), mRNA	
XM_036175	Homo sapiens collagen, type XVIII, alpha 1 (COL18A1), mRNA	Collagen, type XVIII, alpha 1
XM_037087	Homo sapiens ATP binding protein associated with cell differentiation (APACD), mRNA	Homo sapiens mRNA for ATP binding protein, complete cds
XM_037646	Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA	
XM_037965	Homo sapiens chondroadherin (CHAD), mRNA	
XM_038584	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3), mRNA	
XM_039094	Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA	
XM_040037	Homo sapiens adrenergic, beta, receptor kinase 1 (ADRBK1), mRNA	Adrenergic, beta, receptor kinase 1
XM_040385	Homo sapiens S-adenosylmethionine decarboxylase 1 (AMD1), mRNA	S-adenosylmethionine decarboxylase 1
XM_042153	Homo sapiens biglycan (BGN), mRNA	Biglycan
XM_042664	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP), mRNA	Nuclear autoantigenic sperm protein (histone-binding)
XM_044120	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3), mRNA	
XM_045089	Homo sapiens ATPase, Cu++ transporting, beta polypeptide (Wilson disease) (ATP7B), mRNA	ATPase, Cu++ transporting, beta polypeptide (Wilson disease)
XM_045802	Homo sapiens paxillin (PXN), Mrna	
XM_045890	Homo sapiens ADP-ribosylation factor 4-like (ARF4L), mRNA	ADP-ribosylation factor 4-like
XM_045925	Homo sapiens decorin (DCN), mRNA	Decorin
XM_045926	Homo sapiens lumican (LUM), mRNA	
XM_046035	Homo sapiens integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL), mRNA	Integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)
XM_046758	Homo sapiens tensin (TNS), mRNA	
XM_046765	Homo sapiens thymidylate synthetase (TYMS), mRNA	Thymidylate synthase
XM_047231	Homo sapiens fibulin 1 (FBLN1), mRNA	
XM_047719	Homo sapiens transcription factor 7 (T-cell specific, HMG-box) (TCF7), mRNA	Transcription factor 7 (T-cell specific)
XM_047802	Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMTS5), mRNA	
XM_048167	Homo sapiens troponin T1, skeletal, slow (TNNT1), mRNA	Troponin T1, skeletal, slow
XM_048201	Homo sapiens metallothionein 1L (MT1L), mRNA	Metallothionein 1L
XM_049177	Homo sapiens vascular endothelial growth factor B (VEGFB), mRNA	
XM_049518	Homo sapiens intercellular adhesion molecule 1 (CD54), human rhinovirus receptor (ICAM1), mRNA	Intercellular adhesion molecule 1 (CD54), human rhinovirus receptor

XM_049534	Homo sapiens amylase, alpha 2A; pancreatic (AMY2A), mRNA	Amylase, alpha 2A; pancreatic
XM_049690	Homo sapiens coatomer protein complex, subunit alpha (COPA), mRNA	Human coatomer protein (HEPCOP) mRNA, complete cds
XM_049864	Homo sapiens colony stimulating factor 3 (granulocyte) (CSF3), mRNA	
XM_049937	Homo sapiens insulin-like growth factor binding protein 4 (IGFBP4), mRNA	
XM_050846	Homo sapiens Indian hedgehog homolog (Drosophila) (IHH), mRNA	
XM_053809	Homo sapiens similar to chondroitin sulfate proteoglycan 2 (versican) (H. sapiens) (LOC153633), mRNA	
XM_054566	Homo sapiens collagen, type VI, alpha 1 (COL6A1), mRNA	
XM_054686	Homo sapiens caspase 3, apoptosis-related cysteine protease (CASP3), mRNA	
XM_055254	Homo sapiens fibronectin 1 (FN1), mRNA	
XM_058069	Homo sapiens matrix metalloproteinase 12 (macrophage elastase) (MMP12), mRNA	
XM_084239	Homo sapiens retinoic acid receptor responder (tazarotene induced) 2 (TIG2) mRNA, complete cds	
XM_084263	(RARRES2), Mrna	
XM_084285	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), mRNA	Human mRNA for cytochrome c oxidase subunit VIc
XM_084705	Homo sapiens integral membrane protein 2A (ITM2A), mRNA	
XM_085705	Homo sapiens tissue inhibitor of metalloproteinase 2 (TIMP2), mRNA	
XM_086368	Homo sapiens MUF1 protein (MUF1), mRNA	H.sapiens mRNA for MUF1 protein
XM_096277	Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA	
Y00985	Human mRNA for manganese-containing superoxide dismutase	
Y07566	H.sapiens mRNA for RIT protein	H.sapiens mRNA for RIT protein
Y07570	H.sapiens mRNA for PHAPI2b protein	H.sapiens mRNA for PHAPI2b protein
Y08999	H.sapiens mRNA for Sop2p-like protein	H.sapiens mRNA for Sop2p-like protein
Y12692	Homo sapiens mRNA for WNT11 gene	
Y13936	Homo sapiens mRNA for protein phosphatase 2C gamma	Homo sapiens mRNA for protein phosphatase 2C gamma
Y15227	Homo sapiens mRNA for leukemia associated gene 1	Homo sapiens mRNA for leukemia associated gene 1
Z22865	H.sapiens dermatopontin mRNA, complete CDS	
Z50781	H.sapiens mRNA for leucine zipper protein	
Z50853	H.sapiens mRNA for CLPP	H.sapiens mRNA for CLPP

The current invention also encompasses the process of down compression of previously determined 467 genes to a lower number that is still able to characterize the desired number of different cellular status. At present, for the determination of 7 different cell types or development stages, a minimum of 26 spots of different marker genes are preferred, much preferred about 200 such spots. For full information, at least one spot for each of the presently 467 genes (markers) is preferred. A reduction of spot number can be of relevance e.g. if under certain conditions only a small subset of those genes listed in Tab II is required for analysis e.g. in clinical applications. This down compression can be achieved by determining the ratio of actual to target number of genes and then choosing from each cluster accordingly to the determined ratio the necessary number of genes to fulfill the requirement. This process requires to group the number of genes for each analysis of e.g. Tab. I into representative cluster families from where representative genes can be selected. Such clusters families can be determined as shown in Figure 1, namely by grouping clusters together that show a similar expression pattern. For each cluster family a representative number of genes may be chosen according to the compression factor that has been defined. It can easily be seen that for larger clusters like e.g. "A" in Tab I more genes are available to select while in other clusters like e.g. "E" in Tab I less are present. At the end of the process one needs to balance the procedure in order to preserve the characteristics of the expression profile. In order to do so the amount of genes for each analysis should at least be greater than 2 sequences or spots, respectively, of different genes and for the total array at least 30. In order to control such a process classical hierarchical clustering (Stanford) analysis can be performed and checked on graphical presentations like treeview (Stanford). Cluster analysis may group similar expression profiles in families and will allow distinguishing between different cell sources and allows classification of these cell cultures (see Fig. 2). If the cell sources are not properly represented in the cluster analysis it means that the selected marker genes are not balanced.

Example of an cartilage specific micro array structure:

To produce a microarray with printed oligonucleotides sequences of approx. at least 10 mers, preferably at least 25 mers, some sequences of table II need to be further processed. Since some of the determined sequences in Tab II are only expressed sequence tags (herein referred to as EST), they do not correspond to or represent the full-length cDNA. Therefore the EST preferably is BLAST searched with the public database at NCBI and the corresponding full-length cDNA determined. Only by having the correct and full-length cDNA it is possible to design oligomeric sequences that are balanced to each other and minimize any cross reactivity. Exemplary polynucleotide sequences (targets) are provided in the sequence listing of Table III. The cartilage related polynucleotide sequences as e.g. listed in Table III and other polynucleotide sequences known as key cartilage genes from the literature can be immobilized on a substrate and used as hybridizable array elements in a microarray format. Such microarrays can be composed of a subset of oligonucleotides representing e.g. sequences listed on Tab. II but modified to represent only full-length cDNA sequences. The used polynucleotides for the production of such a microarray can either be 50mer or also PCR (polymerase chain reaction) products but at least need to be longer than 10 bases. It should be noted that for microarray production also PCR products from the corresponding determined sequences directly or the full length cDNA can be used and it is not restricted just to oligonucleotides.

Methods to anchor such oligonucleotides or polynucleotides on a solid support are described in literature, together with information on length dependent distances between each oligo or polynucleotides and spots . (see e.g. Principal and Practice, DNA microarrays: gene expression analysis B.Jordan, Springer, 2001)

When polynucleotides are employed as hybridizable array elements in a microarray and depending on the software used, the array elements may be organized in an ordered fashion so that each element is present at a specified location on the substrate. If the array elements are at specified locations on the substrate, the hybridization patterns and

intensities (which together create a unique expression profile) can be interpreted in terms of expression levels of particular genes. This expression profile can then be used and may be correlated with any effect associated with a tissue and/or compound or to be investigated with regard to a specific tissue and/or compound and allows comparison with already existing data.

One of such useful application of using ordered polynucleotides on microarrays is e.g. the comparison of gene expression profiles from a new sample e.g. a tissue biopsy, with already determined characteristic gene expression profiles that are preferably stored in a database. Such stored gene expression profiles are e.g. of major importance if microarrays are applied in the clinic. In this case advantageously a database is set up that stores the corresponding gene expression profiles and advantageously also all patient informations, e.g. history, blood pressure etc. By including all patient data and gene expression profiles in the analysis process and then starting a comparison with an expression profile from a new biopsy, it becomes possible to achieve a stronger correlation with the clinical outcome. This will allow to determine which therapy shall be applied, or even to modify an existing therapy, e.g. to add growth factor x at a concentration y during the *ex vivo* tissue engineering phase. It may also be the case that the biopsy sample will demonstrate a poor gene expression profile that precludes the successful application of a modern therapeutic cell/tissue approach. Such cases would then only qualify for traditional surgical approaches, and hence would not obtain the benefits of the tissue engineering process.

In analogy, the assessment of *in vitro* produced cartilage can also be performed. In the same way as mentioned above cell culture parameters, like e.g. culture media conditions, growth factor concentration, are preferably stored in a data base together with the corresponding gene expression profiles. Comparison of the database entry with new profiles of new samples can then be used to assess the quality of the new *in vitro* produced tissue.

Subject Arrays and their use:

It should be noted that the invention described here is not dependent on any special array format rather than the possibility to select from an extended list of 467 novel key cartilage genes as well as meaningful gene expression patterns. A presently preferred subject array is a novel cartilage specific microarray that includes 187 genes that in the scope of this invention have been determined to be cartilage related and 140 genes that have been connected to cartilage in literature (see also Tab III). Normally, in high-density array procedures up to 10000 genes are usually applied and are not specific for certain applications. As one major general drawback, this results in massive data overflow and impaired data analysis due to difficult data handling and procedures. A preferred array has in its current state a minimal number of 150 genes, presently much preferred at most 333 genes, all of those with demonstrated relevance within cartilage tissue. Another major limitation has become apparent. While the invention WO01/24833 A2 describes a few marker genes associated with cartilage phenotype stability they do not allow to extensively describe chondrocyte cultures in details. No comprehensive classification of the different cell populations and culture conditions is possible as well as no gene expression profile or fingerprint can be achieved. Gene expression profiles determined with a set of genes represented in Tab II may allow to perform a more comprehensive analysis of different cell cultures conditions. Furthermore it may allow to compare and classify different tissue or the result of the different applied cell culture conditions. The above mentioned topics may only be possible with the disclosed invention as outlined within the following applications.

The inventive array CART-CHIP 300 TM may be applied to classify (quality control) any source material, such as human cartilage biopsies, mesenchymal stem cell containing bone marrow aspirate, or pre-chondrogenic cells containing tissue according to pre-defined categories with respect to their capacity to re-build or re-organize a hyaline cartilage-like matrix *in vitro*. A rough subdivision could be for example "A", "B", or "C". While "A" will easily produce cartilage-like matrix, "B" will require special treatment to achieve an implantable construct, and "C" will represent those

cases that do yet not qualify for such a procedure. This biopsy classification system will allow:

- Quality control of the starting biopsy material and therefore optimization of the downstream process regarding e.g. *in vitro* tissue engineering applications
- Diagnostic evaluation of the patient and candidate treatment methods (e.g. CARTIGRAFT™) to ensure a cost-optimized procedure
- Quality control of *in vitro* tissue engineered products

The subject array of the present invention can be employed for all kind of research and developmental studies related to *in vitro* tissue engineering of cartilage. The possibility to assess proliferation, differentiation or re-differentiation as well as de novo matrix formation processes through analyses and comparison of a plurality of key cartilage genes (positive/negative markers) within one single experiment replaces current trial and error approaches and is thus far more rational.

The subject array can be applied to screen all kind of drugs, e.g. hormones, growth factors, within *in vitro* chondrocyte cultures regarding a potential beneficial effect on proliferation, differentiation, de novo matrix formation. The deduced expression profiles can then be compared with existing data of e.g. native cartilage tissue and used to further optimize the process. Additionally the expression profiles can be compared with data from human adult and human infant cartilage to deduce a pathway or a strategy of how to induce more tissue formation *in vitro*.

The subject array of the preferred embodiment is very well suitable to better understand reaction pathways leading to new responses of chondrocytes *in vitro*. Only key cartilage genes comprising the whole spectrum of functional gene categories are to be investigated. This can be used to study the complexity of degenerative cartilage process *in vitro* and the respective influence of potential beneficial drugs.

The subject array may be used to optimize cultures for *in vitro* cartilage formation starting from human cell sources other than cartilage like e.g. mesenchymal stem cells or bon marrow aspirates.

This subject array will be preferably used as powerful alternative for conventional molecular biology tools beside more established histological and biochemical analyses. By focusing on the most prominent cartilage marker genes being either positive or negative, it is possible to characterize cartilage or cartilage related tissues as well as cell cultures thereof. In this respect, the subject array can replace conventional RT-PCR studies performed to check for cartilage marker gene expression, e.g. collagen I versus collagen II, aggrecan versus versican. By applying this subject array the set of markers will be easily increased by simultaneously simplifying the experimental procedure and enhancing the outcome.

The subject arrays of the present invention have several advantages compared to existing microarrays as well as to conventional gene expression tools such as RT-PCR, Northern Blots etc.

Most importantly, the subject arrays are all based on key cartilage genes. Beyond all the key cartilage genes known from the literature (~100-200 genes), 467 additional cartilage relevant genes have been discovered. Thus a significantly increased pool of cartilage key genes exists to choose from for various applications. For instance, to understand degenerative processes as they occur in OA or RA by study of complex biological reaction pathways, it is important to follow expression of a relatively large number of genes.

Examples

The examples are described for the purposes of illustration and are not intended to limit the scope of the invention.

Example 1: Analysis of various human cartilage samples

Useful for characterizing chondrocyte cultures derived from different human cartilage samples (adult and fetal), where adult samples are different with respect to their capacity to form living tissue engineered equivalents under high density culture conditions.

Adult chondrocytes show different gene expression clusters compared to fetal chondrocytes and can be further distinguished from samples that will not produce living cartilage constructs (failures).

Human chondrocytes from adult and fetal articular cartilage
5 were proliferated in DMEM-F12 medium containing 10% FCS over several passages and transferred to pellet cultures (0.5×10^6 cells) in serum free DMEM-F12 medium supplemented with Ascorbate and Insulin medium. Proliferated cells were directly lysed with RLT buffer (RNeasy® Mini Kit, Qiagen) after trypsin release from plastic substrate, shredded
10 (QIAshredder, Qiagen) and kept frozen at -80°C in lysis buffer for later processing. High density pellet cultures were cultivated for 2 weeks if not otherwise specified, subsequently washed with phosphate buffered saline (PBS) and lysed in RLT Buffer (supplied with RNeasy® Kit). Total RNA was isolated from all samples as described in the manual provided with the
15 RNeasy kit and stored at -80°C .

Fluorescent labeled aRNA (amplified RNA) constructs were obtained by *in vitro* reverse transcription of the RNA followed by an *in vitro* amplification reaction.

20

2 μg of isolated total RNA were used per sample to amplify RNA by applying only one cycle of *in vitro* transcription (IVT, Millenium Biologix AG, Application Note).

2 μg of total RNA from each sample was primed with oligo(dT)_{24-mer}
25 (containing a T7 RNA Polymerase Promotor) and reverse transcribed using 400 Units SuperScript II reverse transcriptase enzyme, nucleotides, 5x Reaction Buffer and Dithiothreitol (DTT) as described in protocol provided with the enzyme. For ribonuclease protection 1 μL RNase inhibitor (10 Units) was used to prevent RNA degradation during first strand synthesis. This first
30 strand synthesis reaction was incubated for 1 hour at 42°C .

To the first strand synthesis reaction 93 µl nuclease free water, 30 µl second strand buffer (Invitrogen, Basel, Switzerland) and 1.5 µl nucleotide mix (dATP, dTTP, dGTP, dCTP, 25 mM each) was added.

Second strand synthesis reaction mix was obtained by adding 40 Units E. coli polymerase I (New England Biolabs, BioConcept, Allschwil, Switzerland), 10 Units E. coli DNA Ligase (New England Biolabs, BioConcept, Allschwil, Switzerland) and 2.5 Units Ribonuclease H (Fermentas, Labforce AG, Nunningen, Switzerland). Reaction was incubated for 2 hours at 16°C.

After this incubation step remaining RNA was degraded by adding 7.5 µl 1M sodium hydroxid containing 2mM EDTA (Ethylenediaminetetraacetic acid) for 10 minutes at 65°C. 7.5 µl 1M Hydrochloric acid was added to neutralize the reaction.

The obtained double strand DNA was purified in a QIAquick® PCR purification kit (Qiagen, Hilden, Germany) and concentrated to 7.5 µl. To this concentrated RNA following reagents were added to obtain aRNA synthesis mix: 2 µl ATP (Adenosine triphosphate, 75mM), 2 µl GTP (Cytidin triphosphate, 75mM), 2 µl GTP (Guanosin triphosphate, 75mM), 2 µl UTP (Uridin triphosphate, 75mM), 1.5 µl 5-(3-aminoallyl)-Uridin triphosphate and 2 µl reaction buffer and 2 µl Enzyme mix (both provided with Ambion MegaScript Kit, Ambion, Cambridgeshire, United Kingdom).

This aRNA synthesis mix was incubated for 4 hours at 37°C. Remaining double strand DNA was digested by adding 1 µl Dnase I for 15 min at 37°C. aRNA was cleaned and concentrated with an RNeasy® Mini Kit column (Qiagen, Hilden Germany) and then concentrated to a final volume of 9 µl.

Fluorescent dye molecules were coupled to the reactive aminoallyl groups of the incorporated a 5-(3-aminoallyl)-Uridin triphosphate molecules. One aliquot of either Cy3™- or Cy5™-mono reactive dye (Amersham Biosciences, Buckinghamshire, United Kingdom) was diluted in 40 µl water free Dimethyl sulfoxide. 10 µl of one of the diluted Cy™ mono reactive dyes was added to each sample buffered in 100mM Carbonate

buffer (pH 9.00). Reaction was quenched after 1 hour by adding 10.4 µl Ethanol amine for 15 min at room temperature.

Unincorporated dye molecules were removed by ethanol precipitation. 2 µl Glycogen (Invitrogen, Basel, Switzerland) was added as carrier during precipitation. After precipitation aRNA pellet was washed with 80% ethanol, dried and resuspended in 50 µl 1x Fragmentation buffer (200mM Tris(hydroxymethyl)aminomethane hydrochloride, 500 mM Potassium acetate, 150mM Magnesium acetate). aRNA was fragmented for 35 min at 94°C and placed on ice immediately. Fragmented aRNA was dissolved in 900 µl hybridization buffer.

For denaturation aRNA was incubated for 5 min at 98°C and centrifuged for 30 sec at full speed in a microcentrifuge.

One CART-CHIP™ 300 (Millenium Biologix AG, Switzerland) was placed face down in a standard hybridization chamber. Hybridization solution containing the denatured and labeled aRNA sample was injected using a standard micropipet whereas Cy3™ and Cy5™ samples were hybridized together in one hybridization chamber (Millenium Biologix AG, Switzerland). The microarrays were incubated overnight at 42°C in a PCR thermal cycler (TGradient, Whatman Biometra GmbH, Göttingen, Germany).

After incubation unspecific aRNA probe was washed away with 1xSSC, 0.1%SDS for 5 min at room temperature, followed by another wash step in 1x SSC, 0.1% SDS for 5 min and rinsed with 1xSSC without SDS for 1 minute to remove excessive SDS. 1xSSC was discarded. Remaining 1xSSC buffer on the slide surface was removed by centrifuge the slide for 2 min at 1500 x g.

The dried CART-CHIP™ 300 were then scanned using an Affymetrix 418 microarray scanner.

Expression level raw data for every spot was obtained with ImageQuaNT (Molecular Dynamics). Raw data was normalized by dividing every expression value by total expression value of all spots for every sample and filtered by setting all values below the 25 percentile to the value of this 25 percentile to remove noise (25 percentile threshold).

For each sample (e.g. de-differentiated and re-differentiated chondrocytes) a list of all measured genes was generated. This so called gene expression profile was then used for subsequent analyses.

Further data analysis was performed using either hierarchical clustering with cluster.exe (written by Michael Eisen, Stanford University) or Self Organizing Maps (SOM), such as GeneCluster developed by Whitehead Institute (Massachusetts Institute of Technology, MIT). The settings of the software were optimized until a reasonable number of clusters resulted that were able to represent the comparison thoroughly. In the following example the parameters were as following:

Basic parameters: SOM rows 6; SOM col:4; #epochs=3000; #seeds=1

Advanced parameters: initialization: random vectors; neighborhood: bubble; alpha l=2; alpha f=0.005; sigma l=3000; sigma f=2.

Fig 1 shows a typical result from a SOM analysis with the above mentioned basic parameters, whereas Fig 2 shows an example of a graphical presentation of a cluster analysis and viewed by the software treeview.

Example 2: Quality Control and Human Cartilage Sample Classification

Useful to demonstrate how CART-CHIP™ 300 can be used to differentiate between diverse cell culture conditions, to distinguish different patients, to study the influence of 3D culture conditions and to serve as a quality control tool during any tissue engineering process.

Human chondrocytes isolated from 4 different donors were proliferated over one passage (P1) and then cultivated as high density pellets (0.5×10^6 cells) in 3D culture for 7 and 14 days. RNA samples were taken from proliferated as well as from 3D cultured cells resulting in totally 12 different samples as shown in Figure 8. RNA isolated from this samples was shredded in a QIAshredder (QIAGEN, Hilden, Germany), amplified, hybridized, washed and scanned as described in Example 1.

Data sets for all 12 samples were extracted and normalized as described in Example 1 to perform cluster and SOM analysis as noted below. Cluster analysis was performed using normalized data computed with GeneCluster.

Fig 3 shows a picture of such a cluster analysis for all 12 samples (#1-#12) consisting of 20 clusters (c0-c19)

Every cluster represents a typical gene expression pattern for all 12 samples indicated by a point, starting from sample #1 on the left hand side to sample #12 on the right hand side in every cluster. For example cluster c0 represents the expression level of 104 genes in all 12 samples in a given range indicated by the lines located above and below the computed points.

Another example for gene expression levels that behave similar for different culture conditions and donors are depicted in clusters c3, c4, c9 and c10. Meaning that every subset of the three donor specific points #1-#3, #4-#6, #7-#9, #10-#12 (see Tab V for detailed description) have gene clusters that behave similar in all analyzed samples.

An example of differently behaving genes is indicated in cluster c13, representing 10 genes that behave similar in donor #1 and #2 but show a different gene expression patterns for donors #3 and #4.

More detailed analyses are shown in Fig 4, Fig 5, and Fig 6. The clusters produced in these figures clearly demonstrate differences as well as similarities in cell behavior for either t0, t7 or t14 days, respectively.

Another software algorithm that can be applied for analysis of large amounts of data coming from gene microarrays is called hierarchical cluster analysis, whereas genes and/or different conditions with similar behavior in gene expression are clustered together. All hierarchical cluster analyses were performed using Cluster software described in Eisen et al. (1998) PNAS 95:14863) and displayed using treeview.exe developed by same author.

Fig 7 shows such a cluster of selected genes for all 12 samples analyzed. Every square is representing one single gene

expression value. Different intensity means different expression levels. Dark squares are representing samples without any significant change in gene expression compare to the other samples or patients. Bright squares are indicating samples in which genes are up- or down-regulated relative to other samples analyzed. A so called cluster of genes is a group of genes that behave similar from one donor to the other donors.

Not only genes but also samples can be clustered together. These clusters are called similarity dendrograms, shown in the top part of Fig 7. These tree-like structures illustrates similarities in gene expression between different samples or donors. The closer a sample (#1...#12) is located to another sample in this dendrogram the more similar gene pattern they have.

Interestingly to see is that the seven samples located at the right side of the dendrogram (samples #1, #2, #5, #7, #8, #10 and #11) are clustered together. This samples are representing t0 and t7 conditions as described above (illustrated in Tab V), whereas a cluster of 4 samples in the middle of the dendrogram (samples #3, #6, #9 and #12) are representing only t14 samples. This means a microarray of the current invention is able to distinguish between de-differentiated, proliferated samples (t0 and t7) and re-differentiated samples in a later stage (t14).

An outlier represents sample #4 located at the most left side of Fig 7. which represents proliferated chondrocytes (t0) from donor 2 and could not clustered together with the remaining proliferated samples. Interestingly, this sample that it is not similar to all other proliferated samples (#1, #7 and #10) was impaired with its capacity to form cartilage tissue equivalents following expansion in 2D culture. The biochemical analysis revealed a lower amount of total collagen/DNA for this sample and immunohistochemistry with collagen II antibodies resulted in only weak staining for a collagen II.

Example 3: Aortic Fibroblasts vs. Chondrocytes

Example to differentiate between expanded chondrocytes and aortic fibroblasts cultivated over 14 days in 3D settings.

5 A human aortic fibroblast cell source was proliferated and brought to 3D culture. RNA was isolated after 14 days of culture. Expression data analysis was performed as described in previous Examples 1 and 2 using CART-CHIP™ 300 microarray.

10 A hierarchical cluster analysis was performed as described in example 2. Samples representing 3D culture after 14 days (t14) were included in said data analysis (samples #3, # 6, # 9 and #12, see Tab V).

The result of the described analysis can be seen in Fig 8. The upper part of the figure shows a dendrogram as described in example 2. Aortic fibroblasts are not clustered together with human chondrocytes. The cluster shows a significantly different pattern compared to all other
15 cultures.

Obviously a gene expression pattern of an aortic fibroblast cell source can be clearly separated from a gene expression pattern of human chondrocytes. A micorarray of the present invention is therefore not only able to study differences between different chondrocyte culture
20 conditions but also to distinguish between cells isolated from different tissues.

Example 4: Arthritic conditions vs. healthy conditions

25 Useful to distinguish between normal healthy chondrocyte behavior from cells resembling an arthritic phenotype. Interleukin-1 β is known to play a central role in the inflammation and connective tissue destruction observed in both rheumatoid arthritis (RA) and osteoarthritis (OA). Stimulation of *in vitro* chondrocyte cultures with Interleukin-1 β thus represents a simple experimental arthritis model.

30 The chondrocyte cell source from donor 4 (see Tab V) was proliferated over 3 passages and then cultivated as high-density pellet cultures (0.5×10^6 cells) for 16 hours and 7 days either in the absence or presence of Interleukin-1 β (30 ng/mL). RNA was isolated from all samples,

hybridized to CART-CHIP™ 300 and expression profiles were generated as described in Example 1.

5 A hierarchical cluster analysis was performed as described in Example 1 and the dendrogram and a selection of the representative gene clusters are shown in Fig 9. This clearly shows that already a short stimulus of Interleukin-1 β results in alteration of the chondrocyte phenotype with gene expression changes that can be distinguished from untreated normal chondrocyte cultures.

Appendix**Table I**

Experiment and correlated gene expression analysis	Number of marker genes for each experiment (analysis)	experiment (analysis)
2D marker adult vs. fetal/infant	151	A
2D /3D adult vs. fetal/infant	96	B
3D marker failure	165	C
3D marker adult/fetal/infant	350	D
2D/3D marker adult	48	E
Time dependent failure marker	75	F
3D failure marker	41	G
Apoptosis related failure markers	30	H

5

Table V

Sample Numbers (#)			
	Proliferation (t0)	7 days in 3D culture (t7)	14 days in 3D culture (t14)
Donor 1	#1	#2	#3
Donor 2	#4	#5	#6
Donor 3	#7	#8	#9
Donor 4	#10	#11	#12

10

SOM Description	H4	P2	3D	failure pool	H5	P1	2D	H4	P1	2D	H5	P1	2D	H1	V2	10	H1	V2	10	H1	V2	10	H2	P1	3D	H3	P4	10	H3	P4	10	H3	P4	10	H3	P4	10
2D/2D	0.620146052			0.636013908	0.543651587	0.467426955	0.502962507	0.971864748	7.00E-02					7.00E-02			0.322384183	0.257739798	0.4719374				0.2171374	0.43513725	0.136282818												
2D/2D	1.822807384			1.941662151	1.793508407	2.056234156	2.134502741	2.106181189	1.28342518					1.83140939			1.394248493	0.041624218	1.859400063				1.332666422	0.101879338	1.01879338												
2D/2D	1.422035285			1.871613838	1.941662151	2.056234156	2.134502741	2.106181189	1.28342518					24.22599845			23.2984338	25.57074708	22.01775031				22.57011778	0.286372201	0.286372201												
2D/2D	0.114907897			0.163225522	0.116118632	0.220315232	0.116118632	0.116118632	0.116118632					3.43E-02			9.845115122	0.122245522	0.26907187				0.195719707	0.454974525	0.454974525												
2D/2D	0.152916598			0.163653836	0.40617698	0.40617698	0.40617698	0.40617698	0.40617698					5.081143315			5.971255034	6.851146942	6.851146942				1.524776699	1.004541129	1.004541129												
2D/2D	0.205801155			0.236801155	0.236801155	0.236801155	0.236801155	0.236801155	0.236801155					2.904240444			0.426262021	0.38468951	0.38468951				1.3469481	0.673349554	0.673349554												
2D/2D	0.897114182			13.62628438	14.05576263	12.91542024	10.56526531	11.73429545	11.73429545					11.73429545			11.73429545	9.819378872	9.819378872				8.673349554	8.673349554	8.673349554												
2D/2D	0.345251229			33.26613692	33.26613692	33.26613692	33.26613692	33.26613692	33.26613692					48.33476779			48.33476779	44.52379325	44.52379325				65.92819049	65.92819049	65.92819049												
2D/2D	0.623673424			43.61031332	43.61031332	43.61031332	43.61031332	43.61031332	43.61031332					48.33476779			48.33476779	44.52379325	44.52379325				65.92819049	65.92819049	65.92819049												
2D/2D	0.81389212			56.44454367	56.44454367	56.44454367	56.44454367	56.44454367	56.44454367					48.33476779			48.33476779	44.52379325	44.52379325				65.92819049	65.92819049	65.92819049												
2D/2D	0.639739103			0.639739103	0.639739103	0.639739103	0.639739103	0.639739103	0.639739103					0.639739103			0.639739103	0.639739103	0.639739103				0.639739103	0.639739103	0.639739103												
2D/2D failure vs. cartilage	0.872455407			1.541734461	3.982307846	3.982307846	3.982307846	3.982307846	3.982307846					0.872455407			0.872455407	0.872455407	0.872455407				0.872455407	0.872455407	0.872455407												

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A4634008	8	2D3D failure (pdf)	1.633316095	0.546444823	1.670188138	2.698127971	1.57955189	1.259078761	1.359339321	1.036497507	13.34177466	1.724578212	0.953208694	1.024786523	1.068524094	1.558183928
A463950	8	2D3D failure (pdf)	1.604345905	0.509030623	2.869733356	2.49429374	1.639289394	1.270569777	1.073489887	1.038523555	15.81952721	1.5894376	0.498710814	0.559453728	0.815020682	1.868191082
A467950	3	2D3D failure (pdf)	1.787610548	0.639410548	1.3560157	2.429039394	1.263003994	2.355664222	0.246852478	0.424685652	5.143824512	0.87450181	0.290250889	0.305505421	1.21495112	1.439511082
A4029934	19	2D3D failure (pdf)	2.356686843	1.558646588	2.787420272	2.743130089	2.302306255	2.141115338	10.39261687	6.178828216	3.258015168	2.897213128	3.76309831	6.718135078	4.894432581	4.353783818
A4672597	21	3D addit vs. fctd	17.51963555	30.1489538	29.28930505	30.1489538	24.52945518	17.84179853	48.00745138	36.04780653	38.04780653	60.24320179	47.48182835	40.945671659	25.81671577	48.51971659
A4428185	3	3D addit vs. fctd	5.267867653	8.195557001	7.23507727	7.48271081	5.05992908	5.53076757	5.53076757	5.53076757	5.53076757	5.53076757	5.53076757	4.515305124	3.062554077	4.564261077
A4478724	3	3D addit vs. fctd	3.470387154	4.172043614	5.052765318	5.052765318	5.052765318	5.052765318	2.441015531	4.011719078	1.703891212	1.398038614	2.575869592	1.573760187	1.247483101	2.752822402
T40541	2	3D addit vs. fctd	12.31479553	12.31479553	12.31479553	12.31479553	12.31479553	12.31479553	0.276153908	0.546299287	3.02618974	0.963576817	8.51E-02	8.50E-02	3.92E-02	1.06318934
N33214	2	3D addit vs. fctd	2.05473448	2.05473448	2.05473448	2.05473448	2.05473448	2.05473448	0.13076649	0.257442721	1.248745094	1.248745094	0.15024888	4.35E-02	5.26E-02	1.70833088
W69399	2	3D addit vs. fctd	2.81894785	2.81894785	2.81894785	2.81894785	2.81894785	2.81894785	0.345232348	0.345232348	0.345232348	0.345232348	0.15024888	4.35E-02	5.26E-02	1.70833088
H85454	2	3D addit vs. fctd	1.8852931	1.8852931	1.8852931	1.8852931	1.8852931	1.8852931	0.164232157	0.164232157	0.164232157	0.164232157	0.15024888	4.35E-02	5.26E-02	1.70833088
T11284	2	3D addit vs. fctd	2.476255375	2.476255375	2.476255375	2.476255375	2.476255375	2.476255375	0.323E-02	4.43E-02	4.43E-02	4.43E-02	0.14885169	0.14885169	0.14885169	0.14885169
N95418	2	3D addit vs. fctd	1.583715159	1.583715159	1.583715159	1.583715159	1.583715159	1.583715159	7.17E-02	4.65E-02	4.65E-02	4.65E-02	0.23927882	3.19E-02	1.92E-02	0.40050075
A4430675	18	3D addit vs. fctd	13.5115773	13.5115773	13.5115773	13.5115773	13.5115773	13.5115773	30.86231122	32.28482203	32.28482203	32.28482203	44.48538823	33.27001038	32.81546787	23.4221611
A462851	21	3D addit vs. fctd	17.109521824	33.76884941	28.22129217	28.22129217	28.22129217	28.22129217	48.89243645	47.874881	2.119161429	5.612848593	60.1103483	37.00543355	5.59293453	5.42764127
A447236	21	3D addit vs. fctd	6.68230727	4.73477088	5.98573617	5.98573617	5.98573617	5.98573617	6.130314027	6.130314027	6.130314027	6.130314027	50.80500421	57.54473082	53.89606071	27.20255224
A4100268	20	3D addit vs. fctd	16.73518464	14.16222538	26.2182888	26.2182888	26.2182888	26.2182888	16.98487286	16.98487286	16.98487286	16.98487286	50.26187697	33.9857052	28.202558	27.82261502
A4070897	20	3D addit vs. fctd	21.13330664	16.5080222	30.63855114	30.63855114	30.63855114	30.63855114	14.0748353	14.0748353	14.0748353	14.0748353	41.54702124	34.23348828	28.42844313	25.01170127
R27859	20	3D addit vs. fctd	18.9989765	13.51396253	26.82897423	26.82897423	26.82897423	26.82897423	4.590770914	4.590770914	4.590770914	4.590770914	32.44688223	28.50781769	31.40872082	17.11693598
N71628	20	3D addit vs. fctd	18.60839394	13.51396253	26.82897423	26.82897423	26.82897423	26.82897423	35.0710988	35.0710988	35.0710988	35.0710988	38.2576454	37.7965424	38.44838831	22.42777155
A4464566	20	3D addit vs. fctd	10.6593398	10.6593398	10.6593398	10.6593398	10.6593398	10.6593398	24.59470164	24.59470164	24.59470164	24.59470164	23.61058895	34.11709303	37.1720184	22.29748728
A4043228	20	3D addit vs. fctd	17.97620829	14.19332756	47.83432102	47.83432102	47.83432102	47.83432102	0.287634172	0.287634172	0.287634172	0.287634172	0.11376793	0.103142991	0.10357228	0.411960124
A4478273	19	3D addit vs. fctd	6.50923187	32.17017287	36.30704558	36.30704558	36.30704558	36.30704558	14.0748353	14.0748353	14.0748353	14.0748353	50.26187697	33.9857052	28.202558	27.82261502
H05919	2	3D addit vs. fctd	2.53006988	4.642200838	6.80194724	6.80194724	6.80194724	6.80194724	12.89817272	12.89817272	12.89817272	12.89817272	10.3222448	9.55533334	9.25150054	7.98340929
A4405562	5	3D addit vs. fctd	5.20712978	4.85656473	8.478297419	8.478297419	8.478297419	8.478297419	0.973906438	0.973906438	0.973906438	0.973906438	10.3222448	9.55533334	9.25150054	7.98340929
A4147043	5	3D addit vs. fctd	5.20712978	4.85656473	8.478297419	8.478297419	8.478297419	8.478297419	0.973906438	0.973906438	0.973906438	0.973906438	10.3222448	9.55533334	9.25150054	7.98340929
A4035934	5	3D addit vs. fctd	5.20712978	4.85656473	8.478297419	8.478297419	8.478297419	8.478297419	0.973906438	0.973906438	0.973906438	0.973906438	10.3222448	9.55533334	9.25150054	7.98340929
R00150	5	3D addit vs. fctd	4.215197474	4.38442636	4.860194724	4.860194724	4.860194724	4.860194724	9.835039103	9.835039103	9.835039103	9.835039103	10.3222448	9.55533334	9.25150054	7.98340929
N40451	5	3D addit vs. fctd	5.20712978	4.85656473	8.478297419	8.478297419	8.478297419	8.478297419	0.973906438	0.973906438	0.973906438	0.973906438	10.3222448	9.55533334	9.25150054	7.98340929
A4405748	5	3D addit vs. fctd	5.20712978	4.85656473	8.478297419	8.478297419	8.478297419	8.478297419	0.973906438	0.973906438	0.973906438	0.973906438	10.3222448	9.55533334	9.25150054	7.98340929
A4481110	5	3D addit vs. fctd	5.20712978	4.85656473	8.478297419	8.478297419	8.478297419	8.478297419	0.973906438	0.973906438	0.973906438	0.973906438	10.3222448	9.55533334	9.25150054	7.98340929
A4845167	5	3D addit vs. fctd	3.757328316	2.504624915	4.190714878	4.190714878	4.190714878	4.190714878	12.89817272	12.89817272	12.89817272	12.89817272	10.3222448	9.55533334	9.25150054	7.98340929
A44318	5	3D addit vs. fctd	4.314381512	6.08876062	6.276793492	6.276793492	6.276793492	6.276793492	5.301613977	5.301613977	5.301613977	5.301613977	10.3222448	9.55533334	9.25150054	7.98340929
N92319	3	3D addit vs. fctd	5.51820527	5.094833947	9.501459451	9.501459451	9.501459451	9.501459451	15.71032329	15.71032329	15.71032329	15.71032329	10.3222448	9.55533334	9.25150054	7.98340929
A4187148	3	3D addit vs. fctd	5.51820527	5.094833947	9.501459451	9.501459451	9.501459451	9.501459451	15.71032329	15.71032329	15.71032329	15.71032329	10.3222448	9.55533334	9.25150054	7.98340929
A253413	3	3D addit vs. fctd	5.51820527	5.094833947	9.501459451	9.501459451	9.501459451	9.501459451	15.71032329	15.71032329	15.71032329	15.71032329	10.3222448	9.55533334	9.25150054	7.98340929
A4164582	4	3D addit vs. fctd	6.41575683	6.41575683	6.41575683	6.41575683	6.41575683	6.41575683	10.40223719	10.40223719	10.40223719	10.40223719	10.3222448	9.55533334	9.25150054	7.98340929
A4486357	4	3D addit vs. fctd	5.52121387	6.23452553	8.103530847	8.103530847	8.103530847	8.103530847	9.56251962	9.56251962	9.56251962	9.56251962	10.3222448	9.55533334	9.25150054	7.98340929
A4180742	4	3D addit vs. fctd	5.52121387	6.23452553	8.103530847	8.103530847	8.103530847	8.103530847	9.56251962	9.56251962	9.56251962	9.56251962	10.3222448	9.55533334	9.25150054	7.98340929
A4437268	4	3D addit vs. fctd	5.52121387	6.23452553	8.103530847	8.103530847	8.103530847	8.103530847	9.56251962	9.56251962	9.56251962	9.56251962	10.3222448	9.55533334	9.25150054	7.98340929
A4458849	3	3D addit vs. fctd	5.495285544	3.69373147	4.802306884	4.802306884	4.802306884	4.802306884	6.827076847	6.827076847	6.827076847	6.827076847	10.3222448	9.55533334	9.25150054	7.98340929
A4504891	3	3D addit vs. fctd	5.495285544	3.69373147	4.802306884	4.802306884	4.802306884	4.802306884	6.827076847	6.827076847	6.827076847	6.827076847	10.3222448	9.55533334	9.25150054	7.98340929
A4506955	18	3D addit vs. fctd	5.258170088	8.251213126	6.90322093	6.90322093	6.90322093	6.90322093	30.01080002	30.01080002	30.01080002	30.01080002	10.3222448	9.55533334	9.25150054	7.98340929
A4539158	5	3D addit vs. fctd	5.258170088	8.251213126	6.90322093	6.90322093	6.90322093	6.90322093	30.01080002	30.01080002	30.01080002	30.01080002	10.3222448	9.55533334	9.25150054	7.98340929
A4052922	2	3D addit vs. fctd	4.160294487	2.183565002	2.762893749	2.762893749	2.762893749	2.762893749	2.098691401	2.098691401	2.098691401	2.098691401	10.3222448	9.55533334	9.25150054	7.98340929
A4789328	2	3D addit vs. fctd	3.46804111	3.795346147	3.46804111	3.46804111	3.46804111	3.46804111	3.02115482	3.02115482	3.02115482	3.02115482	10.3222448	9.55533334	9.25150054	7.98340929
A4482629	5	3D addit vs. fctd	5.90039148	4.035111964	6.755224678	6.755224678	6.755224678	6.755224678	5.27050552	5.27050552	5.27050552	5.27050552	10.3222448	9.55533334	9.25150054	7.98340929
H93018	2	3D addit vs. fctd	2.951127838	2.622458107	2.36828532	2.36828532	2.36828532	2.36828532	1.876776497	1.876776497	1.876776497	1.876776497	10.3222448	9.55533334	9.25150054	7.98340929
A4484217</																

AA46400	2	3.306242137	3.22506502	1.474724063	1.474724063	0.631226114	1.560082834	8.474436594	0.43389112	0.405349004	0.482918982	2.543018921	5.42E-02	7.07E-02	5.08E-02	0.744503106
H13991	19	46.00279395	36.30704958	36.30704958	53.01474929	53.01474929	1.60794821	45.61749341	38.06839644	45.61749341	32.30877452	19.69909539	32.30877452	7.07E-02	5.08E-02	0.744503106
AA122066	2	3.357550539	3.293125381	1.567514408	1.567514408	1.567514408	5.862959372	5.862959372	0.38938394	0.152206065	0.357001431	0.989742687	0.102771685	0.210123178	5.56E-02	0.589527392
AA480073	2	4.01494944	4.45269262	4.01494944	4.45269262	3.511334464	4.11888207	5.70873971	0.223043973	0.324501012	1.41227979	0.464995516	1.253748511	1.167165782	0.478969407	1.89302538
AA04945	2	2.154589067	2.251683281	2.251683281	2.251683281	2.251683281	2.251683281	4.559458468	0.28201912	0.237321497	0.257785251	0.256505937	0.537559634	0.252450904	0.128562307	1.01938108
R55706	2	1.851341821	1.851341821	1.851341821	1.851341821	1.851341821	1.851341821	4.559458468	0.137145705	0.933E-02	0.36327564	0.36327564	0.79E-02	2.14E-02	1.16E-02	0.572340722
H50114	2	1.903209722	1.706040938	1.40714465	1.40714465	1.40714465	1.40714465	4.599212608	0.149293742	0.114929742	0.542033448	0.019309383	5.53E-02	1.78E-02	1.81E-02	0.620129597
AA452841	2	1.231373773	1.0248198	0.96383432	0.96383432	0.96383432	0.96383432	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
W73790	2	1.17927735	1.07925971	1.07925971	1.07925971	1.07925971	1.07925971	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA291558	17	1.623942532	1.623942532	1.623942532	1.623942532	1.623942532	1.623942532	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA453787	2	2.09323573	1.709197068	1.44074587	1.44074587	1.44074587	1.44074587	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
H05555	2	2.621892845	1.717335096	1.717335096	1.717335096	1.717335096	1.717335096	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA418177	18	1.65443557	2.582817585	1.31103573	1.31103573	1.31103573	1.31103573	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA458201	2	2.02322463	1.59569735	1.726921373	1.726921373	1.726921373	1.726921373	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA232818	18	15.40443015	27.23128653	27.23128653	27.23128653	27.23128653	27.23128653	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
W44660	17	12.7340551	18.0370743	13.8942187	13.8942187	13.8942187	13.8942187	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA629862	17	1.53737895	1.71229223	1.53737895	1.53737895	1.53737895	1.53737895	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA418764	2	2.543634127	1.427789252	1.00028271	1.00028271	1.00028271	1.00028271	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
T52484	2	2.363098407	1.83920989	1.67002108	1.67002108	1.67002108	1.67002108	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA468233	2	2.80322463	1.59569735	1.726921373	1.726921373	1.726921373	1.726921373	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA468233	2	1.05294328	2.016514163	1.407057553	1.407057553	1.407057553	1.407057553	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA079775	2	3.612629568	2.70567137	3.00950285	2.126182568	2.126182568	2.126182568	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
W73989	2	3.69412557	3.593500644	3.632704149	3.632704149	3.632704149	3.632704149	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
R53307	2	2.28239181	1.89608068	1.46881305	1.46881305	1.46881305	1.46881305	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA468233	2	3.014420759	1.69608068	5.310431247	5.310431247	5.310431247	5.310431247	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
R4821	2	4.81781503	3.60517107	3.184315863	3.184315863	3.184315863	3.184315863	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
R8763	2	1.73898085	2.01677633	1.56423505	1.56423505	1.56423505	1.56423505	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
H69583	2	3.472010108	3.07075833	1.87635005	1.87635005	1.87635005	1.87635005	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
R53046	2	2.875040339	3.636942826	3.134265566	3.134265566	3.134265566	3.134265566	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA822705	2	5.753846636	2.394214943	1.826255564	1.826255564	1.826255564	1.826255564	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA418761	2	2.30046874	1.882161	1.167380172	1.167380172	1.167380172	1.167380172	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA02440	2	4.537574439	2.816687278	2.313438182	2.313438182	2.313438182	2.313438182	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
H2531	2	2.080088468	1.72887256	1.459445529	1.459445529	1.459445529	1.459445529	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA480911	15	28.52959985	38.28250422	40.39486802	40.39486802	40.39486802	40.39486802	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA469082	13	8.937884327	15.05040142	10.82056372	10.82056372	10.82056372	10.82056372	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA679065	17	11.54070082	20.86168208	18.075708	18.075708	18.075708	18.075708	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
R43509	16	9.509595949	15.74133733	14.13918278	14.13918278	14.13918278	14.13918278	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
N87553	16	11.02553598	10.4436779	14.87859684	14.87859684	14.87859684	14.87859684	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA679555	16	8.121810176	9.54784588	12.25345162	12.25345162	12.25345162	12.25345162	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
R14692	2	0.767185559	0.580683899	0.752811699	0.752811699	0.752811699	0.752811699	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA43830	2	1.141747364	1.76881039	1.681839103	1.681839103	1.681839103	1.681839103	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA027540	14	30.77584038	23.6975538	23.6975538	23.6975538	23.6975538	23.6975538	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA456930	14	25.53579208	28.39948893	28.39948893	28.39948893	28.39948893	28.39948893	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA453915	13	8.70806871	16.03563015	13.0174715	13.0174715	13.0174715	13.0174715	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA074448	13	9.620040415	13.82726113	12.87589434	12.87589434	12.87589434	12.87589434	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA027042	13	12.73491005	16.51863878	13.49949447	13.49949447	13.49949447	13.49949447	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA629823	13	11.63735402	10.2004947	10.4861254	10.4861254	10.4861254	10.4861254	4.559458468	0.241515568	0.303697054	0.216412084	0.47235925	0.327239291	0.241219124	0.10455358	0.735173064
AA460630	13	37.95742358	39.37970587	37.95742358	37.95742358	37.95742358	37.95742358	4.559458468	0.24							

AA029604	0	3.855047135	3.855047135	4.014123181	5.758885572	4.613362037	4.007230855	3.687567081	7.965348913	10.02474618	7.993306187	7.553245463	6.00361088	14.22552591	13.76168965	9.150938402
AA482919	0	3.27498817	3.27498817	3.471161389	3.9180529374	3.243068103	3.469093689	3.176498483	3.977660231	4.857158927	3.943713982	3.637640609	5.19250022	4.094539228	4.217440316	3.923350037
AA043133	0	3.039642745	3.039642745	3.471161389	5.203132079	4.221332079	4.258062181	3.176498483	3.977660231	4.857158927	3.943713982	3.637640609	5.19250022	4.094539228	4.217440316	3.923350037
AA012873	17	15.77249197	10.74549128	18.85394679	18.85394679	18.85394679	18.85394679	18.85394679	18.85394679	18.85394679	18.85394679	18.85394679	18.85394679	18.85394679	18.85394679	18.85394679
AA454371	0	3.957168234	3.957168234	3.957168234	3.957168234	3.957168234	3.957168234	3.957168234	3.957168234	3.957168234	3.957168234	3.957168234	3.957168234	3.957168234	3.957168234	3.957168234
AA264693	17	14.4127364	14.4127364	14.4127364	14.4127364	14.4127364	14.4127364	14.4127364	14.4127364	14.4127364	14.4127364	14.4127364	14.4127364	14.4127364	14.4127364	14.4127364
N00281	0	2.89910888	2.89910888	3.05073021	3.05073021	3.05073021	3.05073021	3.05073021	3.05073021	3.05073021	3.05073021	3.05073021	3.05073021	3.05073021	3.05073021	3.05073021
AA029542	0	3.329124505	3.329124505	3.329124505	3.329124505	3.329124505	3.329124505	3.329124505	3.329124505	3.329124505	3.329124505	3.329124505	3.329124505	3.329124505	3.329124505	3.329124505
AA079345	0	4.041814585	4.041814585	4.041814585	4.041814585	4.041814585	4.041814585	4.041814585	4.041814585	4.041814585	4.041814585	4.041814585	4.041814585	4.041814585	4.041814585	4.041814585
AA454879	2	2.84144946	2.84144946	2.84144946	2.84144946	2.84144946	2.84144946	2.84144946	2.84144946	2.84144946	2.84144946	2.84144946	2.84144946	2.84144946	2.84144946	2.84144946
AA147640	0	2.88914818	2.88914818	2.88914818	2.88914818	2.88914818	2.88914818	2.88914818	2.88914818	2.88914818	2.88914818	2.88914818	2.88914818	2.88914818	2.88914818	2.88914818
AA400991	0	7.054093591	7.054093591	7.054093591	7.054093591	7.054093591	7.054093591	7.054093591	7.054093591	7.054093591	7.054093591	7.054093591	7.054093591	7.054093591	7.054093591	7.054093591
AA422058	17	10.9757317	10.9757317	10.9757317	10.9757317	10.9757317	10.9757317	10.9757317	10.9757317	10.9757317	10.9757317	10.9757317	10.9757317	10.9757317	10.9757317	10.9757317
AA030778	0	14.71408325	14.71408325	14.71408325	14.71408325	14.71408325	14.71408325	14.71408325	14.71408325	14.71408325	14.71408325	14.71408325	14.71408325	14.71408325	14.71408325	14.71408325
AA027287	0	6.177662556	6.177662556	6.177662556	6.177662556	6.177662556	6.177662556	6.177662556	6.177662556	6.177662556	6.177662556	6.177662556	6.177662556	6.177662556	6.177662556	6.177662556
AA480094	0	8.19819273	8.19819273	8.19819273	8.19819273	8.19819273	8.19819273	8.19819273	8.19819273	8.19819273	8.19819273	8.19819273	8.19819273	8.19819273	8.19819273	8.19819273
FA0716	13	7.649134152	7.649134152	7.649134152	7.649134152	7.649134152	7.649134152	7.649134152	7.649134152	7.649134152	7.649134152	7.649134152	7.649134152	7.649134152	7.649134152	7.649134152
AA460501	0	7.95009751	7.95009751	7.95009751	7.95009751	7.95009751	7.95009751	7.95009751	7.95009751	7.95009751	7.95009751	7.95009751	7.95009751	7.95009751	7.95009751	7.95009751
N02199	0	9.67626658	9.67626658	9.67626658	9.67626658	9.67626658	9.67626658	9.67626658	9.67626658	9.67626658	9.67626658	9.67626658	9.67626658	9.67626658	9.67626658	9.67626658
AA430404	0	5.038274076	5.038274076	5.038274076	5.038274076	5.038274076	5.038274076	5.038274076	5.038274076	5.038274076	5.038274076	5.038274076	5.038274076	5.038274076	5.038274076	5.038274076
N03868	0	11.09420423	11.09420423	11.09420423	11.09420423	11.09420423	11.09420423	11.09420423	11.09420423	11.09420423	11.09420423	11.09420423	11.09420423	11.09420423	11.09420423	11.09420423
AA260478	7	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749
AA442092	7	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749	9.8398749
AA029644	7	7.79962639	7.79962639	7.79962639	7.79962639	7.79962639	7.79962639	7.79962639	7.79962639	7.79962639	7.79962639	7.79962639	7.79962639	7.79962639	7.79962639	7.79962639
AA461464	0	7.355616049	7.355616049	7.355616049	7.355616049	7.355616049	7.355616049	7.355616049	7.355616049	7.355616049	7.355616049	7.355616049	7.355616049	7.355616049	7.355616049	7.355616049
TA0859	12	7.102239287	7.102239287	7.102239287	7.102239287	7.102239287	7.102239287	7.102239287	7.102239287	7.102239287	7.102239287	7.102239287	7.102239287	7.102239287	7.102239287	7.102239287
AA059550	13	8.978421471	8.978421471	8.978421471	8.978421471	8.978421471	8.978421471	8.978421471	8.978421471	8.978421471	8.978421471	8.978421471	8.978421471	8.978421471	8.978421471	8.978421471
AA070569	13	8.512749427	8.512749427	8.512749427	8.512749427	8.512749427	8.512749427	8.512749427	8.512749427	8.512749427	8.512749427	8.512749427	8.512749427	8.512749427	8.512749427	8.512749427
AA47739	13	13.76266889	13.76266889	13.76266889	13.76266889	13.76266889	13.76266889	13.76266889	13.76266889	13.76266889	13.76266889	13.76266889	13.76266889	13.76266889	13.76266889	13.76266889
H00043	13	11.42545368	11.42545368	11.42545368	11.42545368	11.42545368	11.42545368	11.42545368	11.42545368	11.42545368	11.42545368	11.42545368	11.42545368	11.42545368	11.42545368	11.42545368
AA439410	13	11.0926813	11.0926813	11.0926813	11.0926813	11.0926813	11.0926813	11.0926813	11.0926813	11.0926813	11.0926813	11.0926813	11.0926813	11.0926813	11.0926813	11.0926813
AA443039	0	8.661615881	8.661615881	8.661615881	8.661615881	8.661615881	8.661615881	8.661615881	8.661615881	8.661615881	8.661615881	8.661615881	8.661615881	8.661615881	8.661615881	8.661615881
AA164440	11	17.82989233	17.82989233	17.82989233	17.82989233	17.82989233	17.82989233	17.82989233	17.82989233	17.82989233	17.82989233	17.82989233	17.82989233	17.82989233	17.82989233	17.82989233
AA446453	11	16.53396138	16.53396138	16.53396138	16.53396138	16.53396138	16.53396138	16.53396138	16.53396138	16.53396138	16.53396138	16.53396138	16.53396138	16.53396138	16.53396138	16.53396138
AA060652	11	17.40780225	17.40780225	17.40780225	17.40780225	17.40780225	17.40780225	17.40780225	17.40780225	17.40780225	17.40780225	17.40780225	17.40780225	17.40780225	17.40780225	17.40780225
AA031614	11	20.68635757	20.68635757	20.68635757	20.68635757	20.68635757	20.68635757	20.68635757	20.68635757	20.68635757	20.68635757	20.68635757	20.68635757	20.68635757	20.68635757	20.68635757
R03154	11	15.80928053	15.80928053	15.80928053	15.80928053	15.80928053	15.80928053	15.80928053	15.80928053	15.80928053	15.80928053	15.80928053	15.80928053	15.80928053	15.80928053	15.80928053
AA487452	9	9.471410025	9.471410025	9.471410025	9.471410025	9.471410025	9.471410025	9.471410025	9.471410025	9.471410025	9.471410025	9.471410025	9.471410025	9.471410025	9.471410025	9.471410025
AA44688	13	8.047350014	8.047350014	8.047350014	8.047350014	8.047350014	8.047350014	8.047350014	8.047350014	8.047350014	8.047350014	8.047350014	8.047350014	8.047350014	8.047350014	8.047350014
AA48533	23	6.724440565	6.724440565	6.724440565	6.724440565	6.724440565	6.724440565	6.724440565	6.724440565	6.724440565	6.724440565	6.724440565	6.724440565	6.724440565	6.724440565	6.724440565
FA0254	23	0.402098116	0.402098116	0.402098116	0.402098116	0.402098116	0.402098116	0.402098116	0.402098116	0.402098116	0.402098116	0.402098116	0.402098116	0.402098116	0.402098116	0.402098116
AA171613	23	0.630916304	0.630916304	0.630916304	0.630916304	0.630916304	0.630916304	0.630916304	0.630916304	0.630916304	0.630916304	0.630916304	0.630916304	0.630916304	0.630916304	0.630916304
AA025708	0	103.2882145	103.2882145	103.2882145	103.2882145	103.2882145	103.2882145	103.2882145	103.2882145	103.2882145	103.2882145	103.2882145	103.2882145	103.2882145	103.2882145	103.2882145
AA068527	23	1.350133045	1.350133045	1.350133045	1.350133045	1.350133045	1.350133045	1.350133045	1.350133045	1.350133045	1.350133045	1.350133045	1.350133045	1.350133045	1.350133045	1.350133045
TA4144	23	0.478915725	0.478915725	0.478915725	0.478915725	0.478915725	0.478915725	0.478915725	0.478915725	0.478915725	0.478915725	0.478915725	0.478915725	0.478915725	0.478915725	0.478915725
R14080	23	7.006110394	7.006110394	7.006110394	7.006110394	7.006110394	7.006110394	7.006110394	7.006110394	7.006110394	7.006110394	7.006110394	7.006110394	7.006110394	7.006110394	7.006110394
AA069599	23	0.339332481	0.339332481	0.339332481	0.339332481	0.339332481	0.339332481	0.339332481	0.339332481	0.339332481	0.339332481	0.339332481	0.339332481	0.339332481	0.339332481	0.339332481
AA489201	23	7.761267038	7.76126													

R08976	23	3D edit vs. failure	6.204439487	1.240354192	1.127376445	1.300511748	1.365110688	0.580537573	0.370149717	1.576770394	0.394555828	0.43016572	0.422480014	0.295461934	1.181660079
H64223	23	3D edit vs. failure	7.549550263	0.42423823	0.394125705	0.294425579	1.948943388	0.12255004	7.01E-02	6.84E-02	1.742694009	0.150987538	0.159485208	0.251147304	0.159485208
R58149	20	3D edit vs. failure	2.221889535	2.687386949	2.28349791	0.394436137	6.00466275	0.13945424	0.13035184	0.815295152	0.482753426	0.171693865	0.257175948	3.81E-02	2.131988202
AA454619	20	3D edit vs. failure	2.369393568	3.285062897	2.811568095	3.530544823	6.168078813	3.289336393	3.22993937	1.915196108	1.918796037	2.182506824	3.92242817	3.716886899	5.217536513
H15445	20	3D edit vs. failure	2.706447087	1.45888277	1.45785129	2.021283714	6.313813777	0.120219532	0.11175393	-0.02E-02	0.407455552	4.96E-02	1.52E-02	0.01E-02	0.1455052
AA705925	23	3D edit vs. failure	1.386336788	6.429576977	1.34463513	1.195050104	1.750500104	0.1862793	0.180935538	0.84755028	0.259955331	0.093581122	4.21E-02	2.79E-02	0.674488801
AA191488	2	3D edit vs. failure	4.51014434	2.660001833	1.631970516	0.105306504	16.36219408	0.106325	1.338071481	9.77788082	9.77163194	0.268988511	0.571988082	0.368988511	1.716820958
N84882	14	3D edit vs. failure	12.10839017	0.50595005	0.65682947	0.814517248	3.167263977	0.177514618	0.134938261	0.724810552	0.540552309	0.142619803	8.68E-02	8.34E-02	1.380235206
R45413	7	3D edit vs. failure	28.51852355	1.065046051	0.917798985	0.917798985	6.012824228	0.121785119	0.177384842	0.659081246	2.227675821	8.94E-02	0.189578838	0.639711527	10.4808689
R77283	7	3D edit vs. failure	18.87787659	6.908801459	6.158463331	5.192489359	8.00820403	17.2276128	18.58361324	4.930581246	11.25374013	13.83410333	12.77950208	13.46395842	8.219025894
AA676470	5	3D edit vs. failure	34.64438659	8.74081386	7.58232052	18.43599149	8.233904749	15.01390271	13.59205508	9.447623349	23.31189758	9.086747717	12.4718283	13.46395842	8.219025894
AA423934	23	3D edit vs. failure	23.9461759	12.7974882	18.83195374	25.31283182	18.5015249	30.08495758	24.12482703	36.0837453	38.36393944	30.7535858	30.7535858	28.97187759	18.33190316
W88858	20	3D edit vs. failure	6.50776668	0.824546601	0.62227179	0.583061629	1.705329839	8.40E-02	0.248574868	1.87808441	0.590006881	0.115362035	2.84E-02	1.85E-02	0.530855428
H54023	2	3D edit vs. failure	1.157647486	3.73857043	0.70455272	1.04150726	2.789740103	0.173902417	0.153440018	0.620011724	1.520983442	0.023894127	1.65E-02	1.45E-02	0.702231009
H73924	11	3D edit vs. failure	48.92472569	2.06155548	2.01477414	1.746871803	15.29762827	0.277245311	0.148769574	7.22E-02	5.834545617	0.27271827	7.25E-02	4.39E-02	1.386929307
AA481788	0	3D edit vs. failure	61.20693911	36.30704959	92.5592056	102.048037	54.65301063	69.6570315	37.39817347	42.70517469	58.7167488	64.37630302	40.6576745	57.7884949	23.04551033
AA421431	0	3D edit vs. failure	56.7799786	36.30704959	92.5592056	102.048037	54.65301063	69.6570315	37.39817347	42.70517469	58.7167488	64.37630302	40.6576745	57.7884949	23.04551033
AA416103	23	3D edit vs. failure	7.52704012	0.57104593	0.349889394	0.406883851	1.434663011	0.10436512	7.03E-02	7.95E-02	7.95E-02	7.95E-02	0.14859049	0.125075625	0.63099766
N2646	5	3D edit vs. failure	14.8970988	28.9017212	26.5833088	28.5687265	26.0418343	28.6874003	30.98204311	27.56134068	36.82918822	30.95508803	36.0482224	35.37693112	18.5901759
AA453789	18	3D edit vs. failure	8.495936017	2.23826154	2.572107528	1.932193729	3.23708607	1.80940483	2.822490449	2.812870927	1.74620707	2.577080446	1.4222369	1.240811512	1.93017901
AA488929	18	3D edit vs. failure	9.93736838	2.015089405	1.471073914	1.42082874	5.41055459	0.61842463	0.814412924	0.22281388	0.834682507	0.655222734	0.4622369	0.155952818	0.941925731
R0019	18	3D edit vs. failure	8.391310609	3.988970859	2.35403954	2.279353542	4.872725488	1.10534758	1.501873874	0.865525249	0.74059808	0.58317812	0.733053057	0.733053057	1.849381253
AA457343	18	3D edit vs. failure	8.525464296	1.047037018	0.928042539	1.08277505	1.340631611	0.124035689	0.312887764	0.243939547	0.401768082	0.207652428	0.506081312	0.15684645	0.746649314
AA398774	18	3D edit vs. failure	7.756478417	1.017051748	1.620935977	1.820935977	3.313812045	2.36941611	1.59737302	2.194203628	2.081478452	3.36755825	3.36755825	3.36755825	3.542744541
T88884	18	3D edit vs. failure	8.184665438	3.988970859	2.35403954	2.279353542	4.872725488	1.10534758	1.501873874	0.865525249	0.74059808	0.58317812	0.733053057	0.733053057	1.849381253
AA678404	18	3D edit vs. failure	1.841235561	1.3183711	0.48286355	1.579189807	8.384207138	0.287743257	0.228134482	0.372556888	1.777298332	4.68E-02	5.65E-02	0.041057888	1.288613818
H15747	20	3D edit vs. failure	3.703388787	1.841235561	0.48286355	1.579189807	8.384207138	0.287743257	0.228134482	0.372556888	1.777298332	4.68E-02	5.65E-02	0.041057888	1.288613818
H16359	18	3D edit vs. failure	2.50577016	1.852974132	3.258278898	3.258278898	3.421877151	1.894931477	3.008333781	8.830490394	3.547286301	5.733691715	1.619498817	5.733691715	1.283158823
AA430793	14	3D edit vs. failure	7.487527172	1.952974132	3.3404558	1.2240128	4.341547085	0.389167344	1.09581511	10.64077637	2.384094532	0.15911189	0.66028872	0.277728232	1.189970181
AA484709	18	3D edit vs. failure	7.487527172	1.952974132	3.3404558	1.2240128	4.341547085	0.389167344	1.09581511	10.64077637	2.384094532	0.15911189	0.66028872	0.277728232	1.189970181
H24688	18	3D edit vs. failure	2.682350076	2.682350076	1.92152565	1.98472023	4.014560107	0.201862284	0.218982769	0.751879444	0.818388277	0.153938277	0.734814109	7.89E-02	1.552813702
AA884403	18	3D edit vs. failure	8.508218003	2.40866338	2.28718044	2.281883003	4.451891143	2.10480788	2.672782071	1.300537887	1.089433595	1.738827885	1.274846177	1.24055454	2.873138744
AA404619	19	3D edit vs. failure	11.04039228	0.849034927	0.475063655	0.845471218	2.92914748	0.15138884	3.62385316	0.59941884	0.1831414	0.18224032	0.18224032	0.18224032	0.75943341
AA598811	19	3D edit vs. failure	9.658225618	0.48542718	0.382776293	0.327487582	5.321758	0.330074441	0.22590429	1.350802258	1.655047789	0.200113403	0.185068173	0.124232786	1.678765389
H72875	19	3D edit vs. failure	9.658225618	0.48542718	0.382776293	0.327487582	5.321758	0.330074441	0.22590429	1.350802258	1.655047789	0.200113403	0.185068173	0.124232786	1.678765389
H63361	19	3D edit vs. failure	8.605553016	1.751417848	0.96145731	0.718146053	0.178747728	0.178747728	0.178747728	0.178747728	0.178747728	0.178747728	0.178747728	0.178747728	0.178747728
R38221	19	3D edit vs. failure	8.605553016	1.751417848	0.96145731	0.718146053	0.178747728	0.178747728	0.178747728	0.178747728	0.178747728	0.178747728	0.178747728	0.178747728	0.178747728
R02246	19	3D edit vs. failure	8.722284539	0.689643744	0.430680409	0.314907846	1.628641297	8.20E-02	0.208438723	2.150640832	0.235419744	3.89E-02	2.39E-02	3.21E-02	1.140843868
R51835	19	3D edit vs. failure	3.205091888	0.489133148	0.341800718	0.341800718	0.341800718	0.341800718	0.341800718	0.341800718	0.341800718	0.341800718	0.341800718	0.341800718	0.341800718
R333031	19	3D edit vs. failure	0.309199109	0.871901353	0.871901353	0.871901353	0.871901353	0.871901353	0.871901353	0.871901353	0.871901353	0.871901353	0.871901353	0.871901353	0.871901353
AA412053	18	3D edit vs. failure	6.658763777	1.560529339	3.33301865	1.60001113	3.312435004	0.204788914	0.143840453	0.35745167	1.241813181	0.175293392	0.22193368	0.438145557	1.438145557
AA01887	11	3D edit vs. failure	18.55199165	1.276933043	0.83934093	0.83934093	0.83934093	0.83934093	0.83934093	0.83934093	0.83934093	0.83934093	0.83934093	0.83934093	0.83934093
W81911	18	3D edit vs. failure	9.564497621	1.470028439	0.469817818	0.469817818	0.469817818	0.469817818	0.469817818	0.469817818	0.469817818	0.469817818	0.469817818	0.469817818	0.469817818
AA403552	18	3D edit vs. failure	3.912744879	3.208427825	6.182407855	6.182407855	6.182407855	6.182407855	6.182407855	6.182407855	6.182407855	6.182407855	6.182407855	6.182407855	6.182407855
AA394130	20	3D edit vs. failure	1.959948844	3.999471789	2.792799271	3.380148608	6.892347254	2.91607572	3.076041003	4.428370714	4.75925458	4.7187164	4.531947561	3.70805471	3.70805471
N28884	20	3D edit vs. failure	1.12023555	1.255047137	0.128875927	1.597888392	5.129595529	0.112472811	0.101581989	0.452822211	0.2717084	0.376548847	0.2717084	0.2717084	0.2717084
AA57123	20	3D edit vs. failure	1.372454884	1.737081719	1.805411888	2.242577778	5.776097658	0.216923531	0.155918343	0.364328183	0.72386363	0.193198078	7.45E-02	0.10617339	0.52875191
R43320	19	3D edit vs. failure	0.534524185	0.334762409	0.334762409	0.334762409	0.334762409	0.334762409	0.334762409	0.334762409	0.334762409	0.334762409	0.334762409	0.334762409	0.334762409
AA070430	20	3D edit vs. failure	2.411089781	6.40043776	5.227597585	6.00488788	4.95882131	9.87888888	6.638278632	5.717565814	7.813090558	8.55181804	7.955091885	4.8896271	5.240095284

H5060	3D adult vs. failure	1.02625182	1.323524085	0.84320832	3.42670518	0.34276548	0.256921183	0.586615189	4.289007537	0.478165756	0.479705389	6.74E-02	1.020767749
A445875	3D adult vs. failure	1.073515465	1.016303139	1.117292358	3.660946409	0.765442166	1.506410122	9.808733277	1.82892106	0.920171532	0.658649251	0.698071385	1.594262569
A445871	3D adult vs. failure	1.819694978	1.054175659	1.243382378	4.865742561	0.597819889	1.768417153	11.84393613	2.197826917	0.520943105	0.254992284	0.126606093	1.30740017
T38411	3D adult vs. failure	0.863416806	0.658951165	0.776309726	3.661139864	0.386231188	0.296618072	0.365445552	1.96945161	0.268104021	0.247953039	1.580616835	0.590616835
R00655	3D adult vs. failure	2.760201659	2.808015121	2.780015121	6.090697819	1.097364016	1.02427951	0.765544603	0.973000349	0.539506121	0.142648188	0.154076211	0.154076211
H98666	3D adult vs. failure	3.917391183	3.208047795	4.021338011	2.760491572	1.207706251	1.743619133	1.275714583	1.529882868	1.784602477	2.774146593	1.868370637	3.844830747
H72028	3D adult vs. failure	1.107289228	0.894651185	0.693097551	5.481280912	0.181183944	0.425147123	0.857472955	1.00161974	0.163941215	0.967420557	0.3517793709	0.807758492
A4079177	3D adult vs. failure	0.813601868	0.732792529	0.65486657	3.853148409	0.348135481	0.500333332	1.263826338	4.439877034	0.329343439	0.421138835	0.341562845	1.848279914
N81576	3D adult vs. failure	0.483667061	0.122018711	0.890068809	0.332239214	0.452874405	1.17780513	0.509560351	1.252518701	0.678E-02	2.22E-02	0.94287318	0.94287318
T48657	3D adult vs. failure	0.460548282	0.426598512	0.390972626	5.000691355	0.175402689	0.12813069	0.39315608	0.95324641	0.161388912	0.19676298	0.177052566	1.071322887
N39599	3D adult vs. failure	1.222240919	0.390241865	1.036587917	4.728340078	0.308724868	0.57068457	4.309747618	1.23476181	0.12595577	3.27E-02	1.338939338	1.338939338
R51012	3D adult vs. failure	0.46658518	12.21521754	13.32666832	0.554065456	0.584470801	0.454685202	0.307430002	3.304783027	0.307430002	0.307430002	0.184570106	1.41665339
H90415	3D adult vs. failure	1.027933738	14.40938688	14.40938688	1.543505047	0.913465897	1.116807454	9.244562689	1.997045708	0.350224199	0.10034162	7.87E-02	1.631877709
H41469	2D/3D adult vs. failure	2.097422239	2.097422239	2.097422239	1.728349793	1.413562414	0.118286912	0.15785146	0.540865076	0.105446274	2.38E-02	2.38E-02	0.533593747
W45415	2D/3D adult vs. failure	4.015388257	7.01456083	7.01456083	2.974647228	2.512493348	8.704678808	8.704678808	8.704678808	8.704678808	8.704678808	8.704678808	8.704678808
A447761	2D/3D adult vs. failure	3.707303465	4.799241073	4.799241073	2.225506897	2.437872778	0.786015022	0.528464235	1.211081391	0.239871652	0.17166979	0.272898223	1.005511383
A447486	2D/3D adult vs. failure	4.21930599	0.404576801	0.404576801	3.012632394	2.788948605	0.50108402	1.665300776	0.785265661	0.358207561	0.193783075	0.198174164	1.534418861
R56004	2D/3D adult vs. failure	3.846775908	2.973815371	2.973815371	2.369229598	3.1509812	0.408195453	1.087709289	0.653908131	0.60487088	0.489488914	0.395606236	1.682176599
T65772	2D/3D adult vs. failure	2.538266605	2.538266605	2.538266605	2.643615768	2.482140712	0.25386837	0.25386837	0.25386837	0.25386837	0.25386837	0.116698413	1.388384089
R81295	2D/3D adult vs. failure	5.7522825	3.54542013	3.54542013	1.874728575	1.797286653	7.10615394	0.15780851	0.67401507	0.17757899	6.65E-02	5.00E-02	1.35004744
T81256	2D/3D adult vs. failure	5.260384	1.641968589	1.641968589	1.819566112	1.62956706	2.432404955	1.55948022	0.570424235	0.67401507	8.4E-02	7.32E-02	1.055596815
A445709	2D/3D adult vs. failure	2.090454022	34.42033666	34.42033666	1.664515888	1.304288382	0.139498331	0.33219508	0.250865325	0.189941789	0.189941789	0.189941789	0.189941789
T71079	2D/3D adult vs. failure	4.193722889	4.210242865	4.210242865	1.86551971	1.86551971	0.14439523	0.781888653	1.301612839	0.187224487	9.28E-02	8.82E-02	1.311633115
R5927	2D/3D adult vs. failure	4.828208077	4.383531971	4.383531971	1.682344148	1.25257434	0.10739205	0.534503826	1.752167539	0.187224487	9.28E-02	8.82E-02	1.311633115
A446780	2D/3D adult vs. failure	0.883613375	1.135158078	1.135158078	0.963072645	0.759370468	0.101084793	0.022457683	0.67401507	0.187224487	9.28E-02	8.82E-02	1.311633115
A443613	2D/3D adult vs. failure	1.45288483	19.39007997	19.39007997	0.91028868	0.71908737	1.062812692	0.236488348	2.41641823	0.161958039	0.3988222	0.305725744	1.25699654
A442878	2D/3D adult vs. failure	2.705938237	23.8104244	23.8104244	1.55039764	1.291875843	1.52455491	0.105785367	2.183301764	0.183880227	0.32381001	7.25E-02	0.91181122
A443325	2D/3D adult vs. failure	1.593567836	22.97589102	22.97589102	1.642226165	1.416693191	0.288557525	0.951720085	2.165000865	0.129397588	0.329192564	0.194244938	1.916291602
A445426	2D/3D adult vs. failure	1.389325695	25.67139954	25.67139954	1.27092623	1.068742478	0.988457685	0.871220085	1.661826021	0.2263134	0.184563224	0.121355588	1.266633117
W41785	2D/3D adult vs. failure	1.745341956	1.287689441	1.287689441	3.90501388	1.06742478	1.416492719	0.10470889	2.80711332	0.2805818	0.29084139	2.02E-02	0.98279161
H44082	2D/3D adult vs. failure	1.533032723	28.30131199	28.30131199	1.04758917	1.548633971	1.23686481	0.131630592	0.31775218	0.201302257	9.82E-02	0.376525133	0.503147875
H44467	2D/3D adult vs. failure	1.645750443	22.47803843	22.47803843	0.963072645	0.759370468	0.101084793	0.022457683	0.67401507	0.187224487	9.28E-02	8.82E-02	1.311633115
A444859	2D/3D adult vs. failure	3.124890125	4.592355812	4.592355812	0.899374755	0.899374755	1.880352883	1.594967751	0.345126358	0.345126358	0.345126358	0.121344263	1.87220295
A447838	2D/3D adult vs. failure	1.594102379	1.594102379	1.594102379	1.594102379	1.594102379	1.594102379	1.594102379	1.594102379	1.594102379	1.594102379	0.121344263	1.87220295
A445301	2D/3D adult vs. failure	6.8234592	1.526533929	1.526533929	1.526533929	1.526533929	1.526533929	1.526533929	1.526533929	1.526533929	1.526533929	0.121344263	1.87220295
N69737	2D/3D adult vs. failure	24.90073908	0.393334078	0.393334078	1.094420779	1.094420779	1.094420779	1.094420779	1.094420779	1.094420779	1.094420779	0.121344263	1.87220295
A4488180	2D/3D adult vs. failure	2.115740805	12.05725753	12.05725753	2.115740805	2.115740805	2.115740805	2.115740805	2.115740805	2.115740805	2.115740805	0.121344263	1.87220295
A4457131	2D/3D adult vs. failure	0.152032873	0.207460704	0.207460704	0.207460704	0.207460704	0.207460704	0.207460704	0.207460704	0.207460704	0.207460704	0.121344263	1.87220295
A4479102	2D/3D adult vs. failure	2.285187382	25.01632331	25.01632331	0.885632208	0.885632208	0.885632208	0.885632208	0.885632208	0.885632208	0.885632208	0.121344263	1.87220295
A4456077	2D/3D adult vs. failure	7.731170282	4.509291885	4.509291885	4.761631155	3.981214605	1.594967751	0.345126358	0.345126358	0.345126358	0.345126358	0.121344263	1.87220295
R87487	2D/3D adult vs. failure	7.53857203	3.060217917	3.060217917	3.060217917	3.060217917	3.060217917	3.060217917	3.060217917	3.060217917	3.060217917	0.121344263	1.87220295
A418010	2D/3D adult vs. failure	7.12414318	3.540431767	3.540431767	3.540431767	3.540431767	3.540431767	3.540431767	3.540431767	3.540431767	3.540431767	0.121344263	1.87220295
A4408219	2D/3D adult vs. failure	6.897777687	6.897777687	6.897777687	6.897777687	6.897777687	6.897777687	6.897777687	6.897777687	6.897777687	6.897777687	0.121344263	1.87220295
N74623	2D/3D adult vs. failure	0.685622411	0.685622411	0.685622411	0.685622411	0.685622411	0.685622411	0.685622411	0.685622411	0.685622411	0.685622411	0.121344263	1.87220295
H93984	2D/3D adult vs. failure	4.654446832	3.987945222	3.987945222	3.987945222	3.987945222	3.987945222	3.987945222	3.987945222	3.987945222	3.987945222	0.121344263	1.87220295
A4447684	2D/3D adult vs. failure	14.43816072	4.757378151	4.757378151	2.713135077	2.713135077	2.713135077	2.713135077	2.713135077	2.713135077	2.713135077	0.121344263	1.87220295
A428201	2D/3D adult vs. failure	5.741750046	2.638626534	2.638626534	3.925955597	3.925955597	3.925955597	3.925955597	3.925955597	3.925955597	3.925955597	0.121344263	1.87220295
H9588	2D/3D adult vs. failure	1.454459706	0.93818073	0.93818073	0.93818073	0.93818073	0.93818073	0.93818073	0.93818073	0.93818073	0.93818073	0.121344263	1.87220295
N53512	2D/3D adult vs. failure	1.855890833	27.45755749	27.45755749	1.437831064	1.437831064	1.437831064	1.437831064	1.437831064	1.437831064	1.437831064	0.121344263	1.87220295

0	H27864	0	2D Marker adult vs. field	3.247167731	3.682389404	4.652835461	3.076145132	8.780274543	10.77661553	7.765175273	8.32114728	10.75728456	9.855471293	7.935744552	7.71741053
0	R040457	0	2D Marker adult vs. field	3.328710575	2.77240442	2.855388595	2.393139312	14.72886764	10.72886764	14.72886764	14.8782372	14.8782372	13.4943961	14.6848187	8.891574391
0	R040460	0	2D Marker adult vs. field	2.530276887	2.530276887	2.530276887	2.530276887	14.02000939	13.67188221	8.3259769	8.741227102	13.22366231	14.28706841	14.743181978	0.86039323
1	R06058	1	2D Marker adult vs. field	0.823172955	0.71694884	0.847054285	0.51140685	8.316574942	9.20236521	4.115436741	5.902080978	8.90198442	6.944505085	7.898162293	6.501566894
2	T72022	2	2D Marker adult vs. field	1.353923319	1.353923319	1.353923319	1.353923319	1.353923319	1.353923319	1.353923319	1.353923319	1.353923319	1.353923319	1.353923319	1.353923319
3	R587874	3	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
4	R587874	4	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
5	R587874	5	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
6	R587874	6	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
7	R587874	7	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
8	R587874	8	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
9	R587874	9	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
10	R587874	10	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
11	R587874	11	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
12	R587874	12	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
13	R587874	13	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
14	R587874	14	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
15	R587874	15	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
16	R587874	16	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
17	R587874	17	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
18	R587874	18	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
19	R587874	19	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
20	R587874	20	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
21	R587874	21	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
22	R587874	22	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
23	R587874	23	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
24	R587874	24	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
25	R587874	25	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
26	R587874	26	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
27	R587874	27	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
28	R587874	28	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
29	R587874	29	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
30	R587874	30	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
31	R587874	31	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
32	R587874	32	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
33	R587874	33	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
34	R587874	34	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
35	R587874	35	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
36	R587874	36	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
37	R587874	37	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
38	R587874	38	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
39	R587874	39	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
40	R587874	40	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
41	R587874	41	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
42	R587874	42	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
43	R587874	43	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
44	R587874	44	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
45	R587874	45	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
46	R587874	46	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
47	R587874	47	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
48	R587874	48	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
49	R587874	49	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
50	R587874	50	2D Marker adult vs. field	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271	0.895714271
51	R587874	51	2D Marker adult vs. field	0.895714271	0.895714271										

W7992	19	20	Marker addit vs. total	53.62002013	39.0230655	39.30704958	56.67474828	53.0221611	48.2390911	20.27131765	22.07700187	17.82340894	12.42842429	13.03977086	19.28856463	19.79293359	12.52222224
NT0734	13	20	Marker addit vs. total	50.1395528	37.0196341	39.30704958	48.48333304	47.5751429	45.25023946	16.06076331	22.1813077	13.02269864	16.31280635	19.12043735	16.31280635	19.12043735	16.31280635
H57136	19	20	Marker addit vs. total	12.2328108	9.12487768	36.80704958	8.80535148	11.2531779	10.90399216	23.82858537	23.14775465	17.84717904	22.57191702	27.82017949	19.25424118	19.11363881	16.68407949
AA709414	23	20	Marker addit vs. total	72.81271864	37.61549482	36.80704958	8.80535148	11.2531779	10.90399216	23.82858537	23.14775465	17.84717904	22.57191702	27.82017949	19.25424118	19.11363881	16.68407949
W65401	7	20	Marker addit vs. total	5.47689281	5.67442981	5.42688725	6.078125118	6.04146438	5.62632584	1.582318414	1.02226892	1.02226892	1.02226892	1.02226892	1.02226892	1.02226892	1.02226892
AA435384	15	20	Marker addit vs. total	23.02941313	15.94754038	25.3770515	22.61556554	22.7391169	19.91483801	9.382091141	8.13412308	6.78573609	8.12471674	10.01008974	10.0915221	17.89616882	5.42650573
AA323042	9	20	Marker addit vs. total	8.022234044	8.895662277	9.478217729	9.478217729	9.478217729	9.478217729	9.478217729	9.478217729	9.478217729	9.478217729	9.478217729	9.478217729	9.478217729	9.478217729
AA427725	9	20	Marker addit vs. total	12.69234894	7.55539142	13.07366612	4.261155334	12.4200971	12.81243832	24.1831519	26.60251328	23.95557184	27.8702775	24.29216348	20.94853555	31.50513283	14.02068164
N51280	8	20	Marker addit vs. total	6.832338115	7.385168272	7.40609108	7.785748506	7.785748506	7.785748506	7.785748506	7.785748506	7.785748506	7.785748506	7.785748506	7.785748506	7.785748506	7.785748506
AA1347	8	20	Marker addit vs. total	4.80487592	5.45251025	4.80487592	5.45251025	4.80487592	5.45251025	4.80487592	5.45251025	4.80487592	5.45251025	4.80487592	5.45251025	4.80487592	5.45251025
AA40280	8	20	Marker addit vs. total	4.95153621	4.50182924	4.50182924	4.50182924	4.50182924	4.50182924	4.50182924	4.50182924	4.50182924	4.50182924	4.50182924	4.50182924	4.50182924	4.50182924
N99435	7	20	Marker addit vs. total	7.12540527	6.54112951	7.7721864	6.54112951	7.7721864	6.54112951	7.7721864	6.54112951	7.7721864	6.54112951	7.7721864	6.54112951	7.7721864	6.54112951
AA490229	7	20	Marker addit vs. total	5.803194729	5.02493	4.546705412	6.046321655	6.046321655	6.046321655	6.046321655	6.046321655	6.046321655	6.046321655	6.046321655	6.046321655	6.046321655	6.046321655
W61391	9	20	Marker addit vs. total	7.335226925	7.335226925	7.335226925	7.335226925	7.335226925	7.335226925	7.335226925	7.335226925	7.335226925	7.335226925	7.335226925	7.335226925	7.335226925	7.335226925
NS1018	7	20	Marker addit vs. total	5.488100802	38.59262312	9.317433978	9.317433978	9.317433978	9.317433978	9.317433978	9.317433978	9.317433978	9.317433978	9.317433978	9.317433978	9.317433978	9.317433978
AA45281	7	20	Marker addit vs. total	6.998002782	9.317433978	9.317433978	9.317433978	9.317433978	9.317433978	9.317433978	9.317433978	9.317433978	9.317433978	9.317433978	9.317433978	9.317433978	9.317433978
W69471	7	20	Marker addit vs. total	7.215022787	5.20000085	9.197659311	5.20000085	9.197659311	5.20000085	9.197659311	5.20000085	9.197659311	5.20000085	9.197659311	5.20000085	9.197659311	5.20000085
AA48821	7	20	Marker addit vs. total	6.616843406	3.688421667	10.148224	5.38922281	5.04776773	6.062776617	1.034014618	1.422616774	15.1920754	7.16723464	1.25470041	1.40454396	1.73363881	4.18365485
AA45882	7	20	Marker addit vs. total	6.961286958	6.280975268	6.441469774	7.072822475	7.546598009	6.402438243	5.030129446	5.67117844	1.45626841	1.68375405	1.68375405	2.379538052	4.179216222	4.062391389
AA42095	7	20	Marker addit vs. total	10.53638887	6.89251828	8.035104314	8.53072052	8.715024875	7.553607298	4.829174413	4.615478182	3.252727167	3.668199484	3.668199484	2.808815532	3.659090891	3.355687801
N99003	7	20	Marker addit vs. total	7.777346527	5.123406597	7.271380835	7.694072399	8.01605624	6.947944869	2.039062485	2.56357284	1.92061982	1.456705844	2.0021831	1.983355512	1.593312179	1.593312179
AA409284	7	20	Marker addit vs. total	5.20327651	6.75228727	5.96252818	5.392875592	5.48694016	6.84732468	2.20425229	2.883924258	1.5451555	1.26465436	2.17588501	1.85688897	1.575172599	3.00772428
AA478288	5	20	Marker addit vs. total	4.597623085	4.318668521	6.168419327	3.952137125	6.299163958	4.511434885	31.39371467	32.51612495	19.8194056	22.2287943	29.07492789	24.93265482	25.96878587	17.40551832
AA40883	13	20	Marker addit vs. total	8.710213419	6.63631914	10.89297008	8.897800204	10.76465611	7.594384628	30.84392285	28.66604793	25.6336039	30.51824359	30.3397488	24.55752432	28.9008593	20.25532838
AA48043	13	20	Marker addit vs. total	10.86503107	6.878393398	11.70702321	9.829080466	10.62920807	10.9035389	21.82386831	20.0686984	18.89282319	22.61450267	25.53193168	21.90738168	21.90738168	13.12039825
AA50545	13	20	Marker addit vs. total	6.15908969	7.77474052	10.84632581	7.657846419	7.632324868	5.43221512	23.8360098	22.05445745	18.8398426	18.63355782	20.21765542	23.90922453	31.7331025	17.38904023
AA487893	13	20	Marker addit vs. total	7.08622819	7.08622819	10.38317033	8.16637819	8.67781639	6.54627414	20.27570383	19.61888578	17.2329505	24.0071381	28.53431351	17.78212522	25.91689986	13.82120863
AA282228	12	20	Marker addit vs. total	8.978317165	9.498378167	9.999757753	8.245175408	8.46533271	7.944255354	48.60827655	42.38607553	23.18186775	28.18377651	30.35228689	41.74942514	54.37468139	30.13431188
H97106	9	20	Marker addit vs. total	8.309765669	8.309765669	8.309765669	8.309765669	8.309765669	8.309765669	8.309765669	8.309765669	8.309765669	8.309765669	8.309765669	8.309765669	8.309765669	8.309765669
W98450	12	20	Marker addit vs. total	6.33304604	6.11454874	10.93954818	8.688270747	7.40517824	6.781838425	23.07654727	21.55398888	24.38698954	28.18647168	31.37132599	30.73988527	31.10677394	21.79020978
N33331	13	20	Marker addit vs. total	8.753238045	12.01197759	8.753238045	12.01197759	8.753238045	12.01197759	8.753238045	12.01197759	8.753238045	12.01197759	8.753238045	12.01197759	8.753238045	12.01197759
AA405800	12	20	Marker addit vs. total	6.223232058	6.223232058	6.223232058	6.223232058	6.223232058	6.223232058	6.223232058	6.223232058	6.223232058	6.223232058	6.223232058	6.223232058	6.223232058	6.223232058
T51539	12	20	Marker addit vs. total	6.495900146	6.570559251	9.469029997	8.820284288	9.194419114	5.753462094	28.33940167	25.78662125	25.6507432	23.9119729	29.14739213	20.1376127	23.03401198	15.45020589
NS9764	12	20	Marker addit vs. total	7.60540659	4.758724822	8.39181538	7.278906425	8.193204655	6.251234677	24.30385591	21.24727989	22.53923803	18.07436869	26.90427658	20.95572529	23.22437469	16.44600318
AA621346	11	20	Marker addit vs. total	18.0187463	11.98813391	20.045391947	17.98437255	19.72783582	15.44685686	9.92748243	4.83573541	4.871009817	5.009423654	4.226278818	6.412726238	6.83199433	4.39487318
AA428551	11	20	Marker addit vs. total	9.132344514	13.57793545	12.536771	12.536771	11.3197892	7.564388812	6.860056659	6.387884337	4.74719124	11.70753397	11.70753397	11.70753397	11.70753397	8.624379722
AA48393	11	20	Marker addit vs. total	10.07198453	8.40710185	10.63545398	9.116267349	9.94808682	5.58545107	3.254207402	4.393727488	3.60219876	2.857452654	3.681140068	6.65644423	5.294861541	0.418574791
AA490172	11	20	Marker addit vs. total	8.374768147	1.415297485	17.38713256	12.06048918	8.20046693	6.194780432	8.93846144	2.818134846	16.5930439	4.55242428	4.55242428	4.55242428	4.55242428	5.753606955
AA50477	12	20	Marker addit vs. total	5.417891216	3.05872235	8.09353431	5.203247321	5.828042051	4.859815506	20.27058266	23.61171293	22.9431745	20.83453263	28.05090535	20.61037432	19.18138364	15.10292793